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Fig. 1A

SEQ ID			
NO		1 5	0
208	HCV-1	1a ATGAGCACGAATCCTAAACCTCAAAAAAAAAAACAAACGTAACACCAACCC	3
209	HCV-J	1bA	
210	HCG9	1cC	
1	BNL1	1dGGC	
5	BNL2	1dCC	
9	CAM1078	1eA-A	
11	FR2	1fCC	
	1112		
211	HC-J6	2aAA	
212	HC-J8	2bAAAAAA	
213	S83	2cAT	
214	NE92	2dA	
17	FR4	2fA	
13	BNL3	2eA	
21	BNL5	2hA	
21	PND	ZII	
215	NZL1	3aACTT	
216	HCV-TR	3bACTG-CCA-AACT	
217	NE48	3cACTACGCA-AT	
217	NE274	3dT	
		3eACTACGCA-AGT	
219	NE145		
220	NE125	3fATTG-CCCA-AACC	
	-	0 0	
221	Z4	4aC	
222	Z1	4bA	
223	GB358	4c	
224	DK13	4dCC	
225	GB809	4eTGC	
27	BNL7	4kGC	
226	BE95	5aA-A	
227	HK2	6aACTACGCA-A	,
228	FR1	7aACTACGCA-ATT	
43	VN4	8aACTACGCA-AT	
45	VN13	8bACTGCA	
47	VN12	9aACTACGCA-AA	
49	NE98	10aACT	í



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Fig. 1B

SEQ II)							
NO			51					100
208	HCV-1	1a	TCGCCCACAGGACGTCA	AGTTCCCGGGTG	GCGG'	FCAGATCG	TTGGTGGA	ıG
209	HCV-J	1b	CT-	C-	-T			_
210	HC-G9	1c	CT-		(C	C	-
1	BNL1	1d	CTK-GSNN	NNNN				-
5	BNL2	1d	C	N	-T			-
9	CAM1078	1e	C	C-	-TC	C 		_
11	FR2	1f	CT-	-A	-G(3- -	-G	_
211	HC-J6	2a	T-	C-	(2 	C	-
212	HC-J8	2b	CT-			- 	C	-
213	S83	2c	C	C-	-TC	C- <i></i> -	C	_
214	NE92	2d	C		-TC	C		-
17	FR4	2f	T-			C	C	-
13	BNL3	2e	C			C	C	-
21	BNL5	2h	CT-		-TC	C	C	_
215	NZL1	3a				A		_
216	HCV-TR		AT-					
217	NE48							
218	NE274		T-					
219	NE145	3 e		C-		C		_
220	NE125		C					
		-	_	_		_		
221	Z 4	4a	CA-		-TG	C	C	_
222	Z1		CATTG-					
223	GB358		CT-					
224	DK13		CT-					
225	GB809		CCATT-					
27	BNL7		CCATT-					
	Dit Di					_	Ŭ	
226	BE95	5a			-т		C	_
220	DD33	Ju		•	-		•	
227	нк2	62	AC	- -			C	_
221	IIICZ	- Ou	AC .				•	
228	FR1	7 =	TAT			^		_
220	PKI	/a	IRI	C	`			
43	VN4	8 =	C			~		_
45	VN13							
40	A1AT 2	OD)		 	 .	 	_	
47	VN12	0.5	ATT					_
4/	AIAIA	Эd	M 11	- C-				_
49	NE98	102	CGT-					_
* 7	11070	TUA	CG	nC-				



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Fig. 1C

SEQ ID				
ИО			101	150
208	HCV-1			CCTAGATTGGGTGTGCGCGCGACGAGA
209	HCV-J			CGTG
210	HC-G9			CGG
1	BNL1			CGNNTG
5	BNL2			CGCG
9	CAM1078			AGC-G
11	FR2	1f		CGG
211	HC-J6	2a	-A	
212	HC-J8	2b	C	-CGAG
213	S83			-GG
214	NE92	2d	-A	
17	FR4	2f		-CGC-AG
13	BNL3	2e		-C
21	BNL5	2h	-A	CC-GG
215	NZL1	3.a	-AG	-ACC-T
216	HCV-TR			-ACAGTAC-T
217	NE48	3 c	-AG	CTTAC-T
218	NE274			-AAGTTC-T
219	NE145			-ACA-TC-T
220	NE125			-ACAGT-C-T
221	Z 4	4 3		-CGTC
222	Z1			
223	GB358			-CGTG
224	DK13			·TG
225	GB809	40		GTC-G
27	BNL7			-CGTC-G
226	BROE		•	G3
226	BE95	5a		GATC-G
227	HK2	6a		CC-G
228	FR1	7a		C-T
43	VN4			-GC-C
45	VN13	8b		C-TG
47	VN12	9a	-CA	-AC-TG
49	NE98	10a	GC-AA	-CCAGTAGT-C-C



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Fig. 1D

SEQ ID			
NO			151 200
208	HCV-1	1a	AAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAA
209	HCV-J	1b	
210	HC-G9		T
1	BNL1		ATCGA
5	BNL2		T-ACG-AT-T-T
9	CAM1078		GTGGCAT
11	FR2		
11	FKZ	11	
211	HC-J6	22	
212	HC-J8		TACGTACCG
212	S83		A
214	NE92		A
17	FR4		T-ACG-A-T-AGCA
13	BNL3		TACGATAGCCT
21	BNL5	2h	A
		_	
215	NZL1		ATAAGCACA
216	HCV-TR		CAAACAGC-T
217	NE48		AGC-CGC-GG
218	NE274		AAGCCAACC-GG
219	NE145		AT
220	NE125	3f	AT
221	Z 4		A
222	Z 1	4b	GATCG
223	GB358		
224	DK13	4d	G
225	GB809	4e	GTGGCA
27	BNL7	4k	GTGCA
226	BE95	5a	GATAC-GT
227	HK2	6a	ACGCACGCAAA
228	FR1	7a.	CACGACGCCAA
43	VN4	8a	GCAGCAAA
45	VN13	8b	A
47	VN12	92	GACGG-CAGCAAA
	*****	24	
49	NE98	10a	GCACG



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Fig. 1E

SEQ ID			
NO			201 250
208	HCV-1		GGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGC
209	HCV-J		CT
210	HC-G9		CCAATG
1	BNL1		T
5	BNL2	1d	C-A-TTNNAC-TC
9	CAM1078	1e	AGCAT
11	FR2	1f	
211	нс-ј6	2a	AGCTACTAATGAA-AAAC
212	HC-J8	2b	A-AGCTACCA-TGAAAT
213	S83	2c	A-AGCAACTA-TGAAGAA
214	NE92	2d	A-AGCACTA-TGAA-AAAA
17	FR4	2f	A-AGCGACTA-TGA-GTAA
13	BNL3	2e	A-AGN-NGACTGA-GTAATC
21	BNL5	2h	A-AGCTACTAATGA-GTAA
215	NZL1	3а	GAGACT
216	HCV-TR		CTCGC-T
217	NE48		GTGGACTG
218	NE274		AT
219	NE145		AC-C-AGGAACTGTC
220	NE125		ACAAGCTT
221	Z4	12	GC-AA
222	Z1		GCTT
223	GB358		AAT-TAT
223	DK13		GC-AA-TTTTTT
225	GB809		GCATAT
225	BNL7		GATATAATA
21	BNL /	41	
226	BE95	5a	GC-AACCTGA
227	HK2	6a	GC-ACAAA
228	FR1	7a	TAC-AGACAC-T-GGAC
43	VN4	8a	A-TGC-AC-AAACC-TCC
45	VN13	8b	TGAC-AAACC-TAC
47	VN12	9a	TGC-A-AA-C-AC-A
49	NE98	10a	GCAAT



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Fig. 1F

SEQ ID			
NO			251 300
208	HCV-1	1a	CCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCC
209	HCV-J	1b	AA
210	HC-G9	1c	C
1	BNL1	1d	NC
5	BNL2	1d	AC
11	FR2	1f	CTCA
211	HC-J6		ACGACTCA
212	HC-J8		GCACTT
213	S83		GCTCAGC
214	NE92		GCGCTCAGC
17	FR4	2f	GCGCCTCAG
13	BNL3	2e	GCCC
21	BNL5	2h	GTTTTTT
215	3707.1	٦-	m
215	NZL1		AGCA
216	HCV-TR		TTTTTTT
217	NE48		CTC
218	NE274		-TTTTTT
219	NE145		TCT
220	NE125	3 1	A
221	Z4	4 a	T
222	Ž1		TC
223	GB358		-TTCTAT
224	DK13		TCA
225	GB809		TC
27	BNL7		-TTCTANNTC
	5112 /		
226	BE95	5a	TC-CCTAGGCT
227	HK2	6a	-TTAC
228	FR1	72	TCAC
220	PKI	/α	
43	VN4		-TTA
45	VN13	8b	-TTC
47	VN12	9a	TG
49	NE98	10a	ACG



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Fig. 1G

SEQ II)		
ИО			301 350
208	HCV-1		CGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCG
209	HCV-J		T
210	HC-G9		C
1	BNL1		C
5	BNL2		C
11	FR2	1f	CAATAAA
211	HC-J6	2 =	ATCTCTCTATAC
212	HC-J8		CGTCTAA
213	S83		CTCTCACAAA
213	NE92		AGATACA
17	FR4		GACA-ACAC
13	BNL3		A
21	BNL5		A
. 21	BMP2	211	A
215	NZL1	3a	CGC
216	HCV-TR	3b	TA-C
217	NE48	3c	CTA-ATA-ATA-A-C
218	NE274	3d	CATCTATAT
219	NE145	3e	CAGTACAC
220	NE125	3f	A-ATA-ATA-AT
221	Z4	4a	CGATCTA-ATT
222	Z1	4b	CTCAGTCTATT
223	GB358	4c	AGTCTA-ATTA-A
224	DK13	4d	
225	GB809	4e	CGGTCTT-ATTGC
27	BNL7	4k	CT
226	BE95	5a	AATATAA
		_	a a sam sm as a
227	HK2	6a	CCC-AC
228	FR1	7a	CGATACAC
•	- ••-		•
43	VN4		CGCA-ATA-ACGC
45	VN13	8b	-NCN-GC
47	VN12	9a	N-GCGGAN-GN-GC
49	NE98	1.0-	C
49	NEAR	IUa	<u></u>



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Fig. 1H

SEQ ID			
NO		351	400
208	HCV-1	1a CAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGA	
209	HCV-J	1b TA	
210	HC-G9	1cT	
11	FR2	1fT	T
211	HC-J6	2aCGT	
212	HC-J8	2bTT	
213	S83	2cCTT	
214	NE92	2dCTT	
17	FR4	2fCT-S	
15	BNL3	2eN-NT	
215	NZL1	3aAA	
216	HCV-TR	3bCT	
217	NE48	3cAG	
218	NE274	3dCCAAA	
219	NE145	3eG	
220	NE125	3fCTA	T
221	Z4	4aC	
222	Z1	4b TCA	
223	GB358	4cCT	
224	DK13	4dC	
225	GB809	4eCC	
223	GBOUS	#6CC	
226	BE95	5a TAAAA	T
227	HK2	6a GTG	T
228	FR1	7aCNC-A	
220	FKL	/a C	
43	VN4	8aCA	
45	VN13	8bCCTNS	
47	IDII O	9aCC	
47	VN12	ya <u></u>	



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Fig. 11

SEQ II)		
NO		401	450
208	HCV-1	1a TGGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTGCCAGGGC	CC
209	HCV-J	1b	
210	HC-G9	1cAGAG	·T
11	FR2	1fTAA-	. _
211	HC-J6	2aCTGAGCCTCA	·T
212	HC-J8	2bTGTGGTCA	·T
213	S83	2c	
214	NE92	2dCTGAGTT-TCA	
17	FR4	2f	
15	BNL3	2e	
13	DIVIDO	2e	
215	NZL1	3aTCAA	
216	HCV-TR	3bT	
217	NE48	3cTA	
217	NE274	3dTCAA	
219	NE145	3eTTTGG-ATCG	
220	NE125	3fTTCG-AGTCA	-
			_
221	Z4	4aACG-GGTC	
222	Z1	4bATC	
223	GB358	4cACG-GTTC	
224	DK13	4dACG-GTTCA	
225	GB809	4eACTACG-GTTCA	-
226	BE95	5aTCAGTCA	$\cdot \mathbf{T}$
227	HK2	6aTCGGT-GCTCGGCT	G
228	FR1	7aCTGC-AA-GGGCTGGCT	· -
43	VN4	8aTCTGATGW-GTCGGN	. –
45	VN13	8b -A-AT	
47	VN12	9aATGTCTGGCA	LΑ



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Fig. 1J

SEQ II)		
NO			451 500
208	HCV-1	1a	CTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGG
209	HCV-J	1b	AT
210	HC-G9	1c	ATTA-ACTC
3	BNL1	1d	
7	BNL2	1d	
11	FR2	1f	N-ATTNNNNNNNNNNNNNNN
211	HC-J6	2a	CGA-ACGTT-T
212	HC-J8	2b	ACTTACGA-ATC
213	S83		CCGGAGGA-AT
214	NE92	2d	CGA-AGA-A
15	BNL3	2e	CNGGGA-ATN
17	FR4	2f	CGGGA-AT
19	BNL4	2q	GAT
23	BNL5	2h	GA-AC
25	BNL6	2i	GA-A
23	DIVEO		
215	NZL1		CGACCTGA-AT-TC
216	HCV-TR	3b	CTTGACAT-GGA
217	NE48	3c	CGACTGGA-TTC
218	NE274	3d	CATGA-A-CCTGAA-AT-TC
219	NE145	3e	ĆACGAACCGAA-AT-T
220	NE125	3f	AATGACTGAA-AT
221	Z4		GA-T
222	Z 1	4b	ACCGGAA-TC
223	GB358	4c	ACTTAC-GGA-CTGA-CT
224	DK13	4d	GCT
225	GB809	4e	ACTTAC-GGA-CC
29	BNL7	4k	GA-CT-T
31	BNL8	4k	GA-CT
33	BNL9	4k	GA-TT
35	BNL10	4k	GA-CT
37	BNL11	4k	GA-TT
39	BNL12	41	GA-CT
226	BE95	5a	CACTGACTGGA
227	нк2	6a	CAGACAA-CGGA-CT
228	FR1	7a	TACAA-CGGCTC
43	VN4	8a	TNNCA-CGNATCN
47	VN12	9a	NATACCA-CGGA-A
51	NE98	10a	AA-TT-TC



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Fig. 1K

SEQ ID			
NO			501 550
208	HCV-1	1a	GAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTCTT
209	HCV-J	1b	TGCGCT-ATTG
210	HC-G9	1c	T-GCTAC-
3	BNL1	1d	T-GCGC-
7	BNL2	1d	TT-G
11	FR2	1£	NCTNT-A
211	HC-J6	2a	T-ACGCTT-GGC-
212	HC-J8		TT-ACTT-GTTGA-
213	S83		TT-GCTCTCT-G
214	NE92		T-GCCTT-ATA
15	BNL3		C
17	FR4		T-GCCTT-GTCT-G
19	BNL4		TGTGTG
23	BNL5		TGCCTT-GTAC-
25 25			G
25	BNL6	21	G11111
215	NGT 1	٦-	T-GCCTTTT
215	NZL1		T
216	HCV-TR		TT-ACTT-GTCTA-
217	NE48		
218	NE274		TT-AC
219	NE145		T-GTTGA-
220	NE125	31	TT-GC
221	Z4		TATTG-
222	Z1		TATG-
223	GB358		TCT-CTATTG-
224	DK13		TC
225	GB809		TCC
29	BNL7		CC
31	BNL8		CTACG-
33	BNL9		TC
35	BNL10		TACYTYATG-
37	BNL11	4k	YCC
39	BNL12	41	A-CA-TG-
226	BE95	5a	TT-ACG-
227	HK2	6a	TCCG-
228	FR1	7a	TCT-AAT-AG-
43	VN4	8a	TG-
47	VN12	9a	TATG-
-,			
51	NE98	10a	TT-AA-



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Fig. 1L

SEQ II NO 208	HCV-1	551 1a GCTTGACTGTGCCCGCTTCGGCCTACCAAGTGCGCAACTCCACGGGGCTT
209	HCV-J	1b -TCA-CACTG-GGTGT-CA-A
210	HC-G9	1cCACTGT-GGTTG-G
3	BNL1	1dG-TAA-KA-CTCG-GG-AT-CG-G
7	BNL2	1dGTAAA-CTC-TG-GG-AT-CG-A
11	FR2	1fC-CACTTG-GAG-A-AC-ATGGC
211	HC-J6	2aA-CCACCG-TCCTGC-GAAGATGTACCGGC
212	HC-J8	2bG-CAA-TGTAGTGGCA-GATT-GTTCTAGC
213	S83	2cA-CTA-TCGTGG-GCAAGGAGGC-ACTCC
214	NE92	2d -TA-CG-TCC-GTGGCAAGAGCA-CTC-
15	BNL3	2e -TG-CCT-TCT-N-GTTG-GCAAATAGTCA-GCC
17	FR4	2f -TA-CCTGTATAGTAAGAAGCCACT-C
19	BNL4	2g -TG-CCT-TCTGTGGTAAGAGTACCA-G
23	BNL5	2h -TC-CG-GCTGTGGCAAGAGCCACTC-
25	BNL6	2iA-CCG-TCTGTGTGCGCGGTTTC-
215	NZL1	3aA-T-CATAAG-CAGTCTAG-GTGGTA-GT-TCC
216	HCV-TR	3bTGCGT-GTAG-GTACACGA-GT-TCA
217	NE48	3cGTCTGTTAG-A-GGCT-G-GTACGTGTAT-CCC
218	NE274	3dGTCTGTTG-A-GGATTGTACGTGTGT-TCC
219	NE145	3eGT-TGCTAGTC-GG-TGG-GTG-AT-CTC
220	NE125	3fGT-TCCAGGGCTAG-GTACA-GA-GT-CCA
221	Z 4	4aC-CTAGTG-GCTACGTG-TTCA-C
222	Z 1	4bCAACAAATGTGCTACGTG-TTCG-C
223	GB358	4cCTA-CGT-A-CTATTGTCA-C
224	DK13	4dCTA-CTATAG-TTG-C
225	GB809	4eC-CTGG-GTTA-CTATTG-TTCG
29	BNL7	4kCCAT-A-CTATTGT-TCA
31	BNL8	4kCTATTA-CTACA-TCA-C
33	BNL9	4kCCA-C
35	BNL10	4k -TCCA-CTA-CTATGT-TCA-C
37	BNL11	4kCCAAC-A-CTACTGT-TCA
39	BNL12	41CCA
226	BE95	5a -TCCTGCTAGTT-CCTACATGT-TA
227	HK2	6aC-CAACATCTTACCTACGGTA
228	FR1	7aC-CACAACAAATTCAAGGT-TA-C
43	VN4	8aC-TAACAACCGGCGTTATACAAGT-TCG
47	VN12	9aC-CCACTCCACTAA-CTATGCTAAGT-TG
51	NE98	10aCT-ACAA-AG-C-GGCTGG-GTACTTGT-CAC



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Fig. 1M

SEQ ID)		
NO		601	650
208	HCV-1	1a TACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTACGAGGCGC	3 C
209	HCV-J	1bTAAAA	
210	HC-G9	1cTA	-A
3	BNL1	1dTTCCTT-CCCA-CTAT	-A
7	BNL2	1dTTCCTT-CCCA-CTAT-A	
11	FR2	1fTTCTT-CGGCCCATAA	
11	TKZ		<u> </u>
211	HC-J6	2aATGGCCA-CTGATCACC-GGC-ACTC	CA
212	HC-J8	2bTCTT-AAACCCACC-GGCCTCA	f –
213	S83	2cATGCCGCT-CT-CCT-GGCCTT-	-A
214	NE92	2dATGACAGAGTCCC-GGCCTCA	\G
15	BNL3	2eTATG-CAC-CT-CAACCCA-GGC-ATT	-N
17	FR4	2fATG-CGTCTG-CTGACCCC-GGCCTCA	
19	BNL4	2gATG-CACTT-CAACCCA-C-GGC-AAT-C	
23	BNL5	2hTATGGT-AAGCCC-GGCCTTA	-
25 25	BNL6	2iATGGT-GAGCCT-GGCCTC-	
23	риго	21 AIGG	·A
215	NZL1	3aGT-C-TCCTT-CTAGC	-A
216	HCV-TR	3bTGTGC-TCCTTGGC	·A
217	NE48	3cATACCTT-GAGCCATC-	- A
218	NE274	3dGTGCCCTGGCCTCC	
219	NE145	3eATGCCT-AAGCCAAT	
220	NE125	3fATAC-TCCTAGCCCTT-	
220	NEIZJ	JI AIACI C C I AGC C C I I	A
221	Z4	4aTATGTCACTAT-	- Δ
222	7.1	4bTT	
223	GB358	4cTACGCAA-C-	
223	DK13	4dTCGCACTAA-C-	
		4eTACCGTGCACAC-	
225	GB809		
29	BNL7	4kT-TCATC-	
31	BNL8	4k	
33	BNL9	4kTTACCCGTACATC-	
35	BNL10	4kTCGTACATC-	
37	BNL11	4kT	
39	BNL12	41T-C-CC	·A
226	BE95	5aTTTATTCCACTA-	. א
220	5633	Ja11	· A
227	HK2	6aTCA	·A
228	FR1	7aTC-TCT-GAACCCT-TT	·A
			_
43	VN4	8aTCCCAGCCCTT	·A
47	VN12	9aTTC-ACAGCCT	Δ
7,	*1417	Ju 1 10 h C Lindo C	
51	NE98	10aATGATCCAGGGTCTC-	·G



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Fig. 1N

SEQ ID)	
NO		651 700
208	HCV-1	1a CGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCA
209	HCV-J	1b GCATGACCGCCGA-T-
210	HC-G9	1c GA-CCTGATCTGCTGC-AAC
3	BNL1	1dG-ATGATACAGCGAT-
7	BNL2	1d T-G-ATGTG-CATGCGAA
11	FR2	1f GCATTGTNGCA-AGA
	1112	
211	HC-J6	2a G-CTGCGTCC
212	HC-J8	2b TCAG-TCTCTTAAT-AGAATAATG
213	S83	2c A-GAAG-GTTAT-AGACC-C
214	NE92	2d GTG-TTGTCCT-AGGAGA
15	BNL3	2e GCGG-GTTGTTATCAGAA-AGCTC-G
_		2f GCGG-GCTGTTATCT-AGA-GTCAT-
17	FR4	
19	BNL4	2g G-GCGG-GTTGTTATGT-AGTTGC
23	BNL5	2h GTG-G-TGTCTAT-AT-AGA-GC-CCAA-
25	BNL6	2i GGGTGTCTATTCT-AGT-GAA
215	NZL1	3a TTTACCTATC-AGC
216	HCV-TR	3b ATGTTTACAGCCACAACC
217	NE48	3c -CTTTGCTACC-AAA-CAAT-
218	NE274	3d TA-TTTGATTGCAATCA
219	NE145	3e ATGTGTTTCG-AGA-C
220	NE125	3f TATTGCCTGCACCT-
221	Z4	4a -CCAATTGACTGATGACTG-
		4b GC-CCAATTGATCTGACGACIG-
222	Z1	
223	GB358	4c GC-CCAACTCATT-ACGA-G-TTG-
224	DK13	4d TT-CCAT-ACTCATGA-GAG-
225	GB809	4e -ACAT-ACTCAACTGAAGACCG-
29	BNL7	4k -CCATCTCATGCGA-AG-
31	BNL8	4k -C-CCATCTATGCGA-AACTG-
33	BNL9	4k -CCATTCTCATGCGA-A-TG-
35	BNL10	4k -CCAT-AGCACTATGCGA-A-TG-
37	BNL11	4k -CCATCTAAGCGAAAA-
39	BNL12	41 -CCAT-ACTAATACTGAAGACTG-
226	BE95	5a TA-CCTGAG-ATTGTCATGACAT-
227	нк2	6a T-C-ATGTTTTGTAT-GTGA-G-TC-ATG
228	FR1	7a GACCATGATCTATTATA-CAAG-CG-
43	VN4	8a GACACTGTTTTGTT-ATGAAGRT-RA
		on different to a second to the second to th
47	VN12	9a T-GCATGTCTCTCGAAGACC
- 1	MEGO	10- C NOTE C MON TO C N CONCO
51	NE98	10a GATTCTTATCTCACTCT



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Fig. 10

SEQ II)		
NO			701 750
208	HCV-1	1a	ACGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGAT
209	HCV-J	1b	-TTTCC-TCAC-CTCC-CGGA-C
210	HC-G9		CT-CC-T-GTCAG
3	BNL1		CATCTCC-CCAC-CC-TGGTAAA-Y
7	BNL2	_	T-TTC-TCAC-RC-CC-TGGTAAC
11	FR2		-TATCC-TCACC-CCCAG-GCATC
11	FK2	11	-1A1CC-1CACC-CAG-GCA1C
211	HC-J6	2a	-TA-ATCCA-ACG-CT-AG-ATGTGCA-C-G
212	HC-J8	2b	G-AT-CATCA-ACAAG-AAC-ACTGTG-AAC-C
213	S83		TTC-ACG-TGC-ATC-CTATC-A
214	NE92		ATACC-CA-ACG-TT-GC-ATA-ATGTGCC-A
15	BNL3		GTCGG-TCCACA-CCCT-GC-ACA-AGTGCA-A
17	FR4		-TAGGA-CTTCACAG-CT-GC-ACTGTGCCGA
			-TAAGCCA-ACG-CTC-ACTGTG-ACC-G
19	BNL4	•	
23	BNL5		-TCAGTC-CCA-AC-TGAC-ATGTGCC-A
25	BNL6	21	ACC-CCA-ACG-CACA-CTGTGCC-A
215	NZL1	2.2	-TA-AT-CCACCC-AGAAAGTT-C
			CAAATCACACAAG-CT-AA-GGTTACC
216	HCV-TR		
217	NE48		AACCA-ACGTGAGGTTC-C
218	NE274		TCAACA-TCGG-AAAGGTT-A-T-C
219	NE145		A-AGACACCCGCAAAGTAT-C
220	NE125	3£	CAGACAC-C-AG-AAGATGTAAC
221	Z4	1.5	A-AC-TCAC-CGGATGT-GCAC-C
222	Z1		-TA-TTC-CCCC-C-TG-GCCCT
223	GB358	_	-TCAGAC-CCCC-CTCCGG-GCCTT-C
224	DK13		AAGT-CACT-TC-CCCTG-GCAAC
225	GB809		CAGCCC-CTCAGT-GCCTT-C
29	BNL7		-TCAGAC-TCACC-TCCAG-GCCAT-C
31	BNL8		-TCAGAC-TCCC-TTCCAG-GCCAT-C
33	BNL9	4k	-TCAGTCCC-TCA-CAG-GCCAT-C
35	BNL10	4k	CAGAC-CCCC-TCCAG-GCCAT-C
37	BNL11	4k	-TCATAC-CCCC-TCCAG-GCCAT-C
39	BNL12	41	A-TC-CCCT-AACG-GCCCATA
226	BE95	5.5	-T-TGAGTACCCAATACT-AGCC-AGC
220	DEJJ	Ja	1-10A01 A C CCAA 1 AC 1 AO CC AOC
227	HK2	6a	-TCGGC-CCCATTGCCCTACCAA
		_	
228	FR1	7a	-T-AGAC-AC-CC-TG-CTC-CT-AGT-CCCA-C
43	VN4	8a	-TCAACCCA-GCCTGCCAGTGCC-A-C
47	VN12	9a	CTGA-C-ACTGCCTGATGGTGCA-A
-1	NEGO	10-	
51	NE98	тuа	-TA-AAACA-CC-TGGYCCGTG-A-TCG



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Fig. 1P

SEQ ID			
NO			751 800
208	HCV-1		GGCAAACTCCCCGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGG
209	HCV-J	1b	AGCAA-CACAA-ACGTCT
210	HC-G9		TCGCGCGTC-GTGGGTGCTC-A
3	BNL1		-CT-GTGA-TRGCAA-CGCTT
7	BNL2	1d	-CTTGTA-TGGCAA-CCTGCTGT
11	FR2	1f	-CGCGCTATCGATGG-GGGCCCG
211	HC-J6	2a	CC-GGCGCT-ACA-GGCT-AGACGTCAGGAT
212	HC-J8		CGGTGCG-T-A-TCGTAGCGACAGCAA-CAAT
213	S83		CCTGGCGCT-T-A-T-A-GGCGGCAA-CA-CGAT
214	NE92		CCTGGTGCG-TTA-C-A-GGCGGACGTTACCA-CA-T-C
15	BNL3		CCTGGTGCT-T-A-C-A-GGAGGGCA-GTGCCG-CGAT
17	FR4		CCTGGTGCT-T-A-T-GAGGTGGGCTACCA-CGAT
19	BNL4		CC-GGCGC-T-A-T-G-GGCT-GGACGTCACCA-CGAT
23	BNL5		CCTGGCGCG-T-A-C-G-GGTT-GGACGTCACCA-CT-C
25	BNL6		CCTGGCGCG-TTA-C-A-GGCGGACATTCA-CAC
215	NZL1		-T-GG-GCAA-TA-TG-TTC-A-ACATG-GCAT-AA
216	HCV-TR		CTTGGCG-GAA-CGTC-A-CACCTG-GAGA
217	NE48		-T-GGTGCGAA-CG-ATC-A-CCG-G
218	NE274		-CTGGCGCGAA-TG-ATC-A-CCATG-G
219	NE145		-CTGGTGCAA-GAG-TTCCG-ACG-AG-GTA
220	NE125		CCTGGCGCAGT-A-CG-ATCAA-CCA-GTG-GTA-GG
220	NEIZS	31	CCIGGCGCAGI-A-CG-AICAA-CCA G IG G I A G G
221	Z4	4a	CCGGGCGCTGCTTGA-TC-T-CGATG-GCT-AA-GA
222	Z 1	4b	CCCGCAGTTAGA-TCCA-GCA-GTG-ACA-GG
223	GB358	4c	AT-GGCGCTGCTTGAATCCCGATG-GA-GA
224	DK13	4d	CTGTGCTGCTTGA-TCTT-GAG-GA-GG
225	GB809	4e	-T-GGTGCTGCTCGACCT-GGCTG-GCA-GA
29	BNL7	4k	AT-GGCGCGACTTGA-TCTAGATG-GCTA-GG
31	BNL8	4k	AT-GGCGCAGCTTGA-TCTGGATG-GA-GG-
33	BNL9	4k	AT-GGCGCAGCTTGA-TCCT-GGATG-GA-GG-
35	BNL10	4k	AC-GCGGCGGCTTGA-TCCGGATG-GA-GG-
37	BNL11		AT-GGCGCGACTTGA-TCTAGATG-GGA-GG
39	BNL12		CTTTCGGCTACTT-T-TCCG-AGGTG-GA-GG
226	BE95		CT-GG-GCAGT-AG-T-CTGA-AGC-G-TCTACA-CG
227	нк2	6a	-CTTCCACGAGGAT-CCA-GTG-GTCG
228	FR1	7a	TCATC-G-GAATCCACGG-TCAG-ACCT
43	VN4	8a	-CGTCTACGA-TCCGG-T-CCAAATG-GCA-CA-GG
47	VN12	9a	-CGTCGG-GTATC-G-GGTG-CCGAGG-GCCT-GG-
51	NE98	10a	CC-TGCGC-GA-CG-CTCTCCACGG-GAA-GG



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Fig. 1Q

SEQ ID		1	801 850
208	HCV-1		GAGCGCCACCTCTGTTCGGCCCTCTACGTGGGGGACCTATGCGGGTCTG
209	HCV-J		-GCGTG-T
210	HC-G9		-GCTG-GTCCA
3	BNL1		-G-NNGTCTA-GRT
7	BNL2		CAG-GT-TCCTA-GCAC-
11	FR2	1f	-GCAGTGTCAA-GA-TTTGGC-
211	HC-J6		-TCCCTTCTGGG-
212	HC-J8		-GCATGGCCT-GTATG-GG-C-
213	S83		-TCTTGGTTTG-GC
214	NE92		ATCTGT-TCTGA-AAAGTCG-G-
15	BNL3	2e	-TCATG-GCG-A-
17	FR4		-TCCTAA-ACG
19	BNL4	2g	-GTTGTAA-CG-GTCG-G-
23	BNL5	2h	-TCTTGCATT-GTCT-CCG-A-
25	BNL6		-TCGTCTT-GT
215	NZL1		CGCGGA-GCTGTTA-GTG
216	HCV-TR	3b	CGCACGACAAGGGCGCT-TG
217	NE48		T-CGTAT-GATCTG-A-
218	NE274	3d	AGCTTGT-GCCGGTTCTA-GTAG-C-
219	NE145		CTTGCGTCTG-C-
220	NE125		TGCAG-GA-AT-T-A-TT-GG
221	Z 4	4a	CGCGTT-GTTTCAGG
222	Z1	4b	TGCGTTA-GCTA-TATGTAGGC-
223	GB358	4 C	TGCTTGCGCCTTA-CAGTGGC-
224	DK13	4d	CGA-CAG-GTGG
225	GB809		TGCTG-GCC
29	BNL7		-GCTG-TATA-CTT-RTYGGCT
31	BNL8		-GCTTG-TCATT-G-TCGGCT
33	BNL9		-GCGTGATA-CTT-GTCGG
35	BNL10		AGCTTG-TATA-CYT-GTCGGCT
35 37	BNL11		-GCTTG-TATA-CTGTGGCT
_			TGCATA-CGTTACGG
39	BNL12		
226	BE95		AG-GTGG-AC
227	HK2	6a	CGCAGTGG-TCATGA-CGTCC
228	FR1	7a	-GCAGG-AT-TA-GA-CACTTAGCA
43	VN4	8a	CGCTG-GTATA-GTGGCC
47	VN12	9a	TGCTTG-GTCTA-GCTTGGGC
51	NE98	10a	RGCGTACATAATTAG-GC



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Fig. 1R

SEQ ID			
NO			851 900
208	HCV-1	1a	TCTTTCTTGTCGGCCAACTGTTCACCTTCTCTCCCAGGCGCCCACTGGACG
209	HCV-J	1b	-TA-TC-CGT-TGA
210	HC-G9	1c	CAT
3	BNL1		CC-CTGATAC-CATGCATA
7	BNL2		C
11	FR2		CCTGTA-GTCGT
11	rkz		A GI C G I I I I I I I I I I I I I I I I
211	HC-J6	25	-GA-GCA-CGATTGGACAATTT
212	HC-J8		-GA-GAC-ATCGGGCTTGG-AA-ACAAAACTTC
212	S83		-GA-GG-CCTGG-CGGT-G-GACAA-ATAC-TTT
	NE92		-GA-GT-G-CTTCTG-CT-AGCAATTAA-TTT
214			-GA-GA-A-CT-CAGGCTT-G-GG-AG-AT-ACTTC
15	BNL3		
17	FR4		-GA-GA-A-CA-CGG-TGC-GT-GAGCAATATACTTTT
19	BNL4	- 3	-GA-GA-A-CT-CTGG-TGTTGGGCAA-ATAACTTT
23	BNL5	2h	-GA-GT-GTCTT-TTGAC-TCAAATCTTC
		_	
215	NZL1		CGAGCCGAGATC-ATCAA
216	HCV-TR		-GAGATC-CACC
217	NE48		-TCCAAGCAAAGAC-ACAA
218	NE274		CT-GGAGGCTAGATC-T-AGAAC
219	NE145 .		CGGGGCCTAAGGTC-TTTACT
220	NE125	3f	-TCGGCTAGAG-TCAAT-ATC
221	Z4	4a	CCGA-GGGAATTCGGGC-TC
222	Z1	4b	CAGGACGAGC-CGC
223	GB358	4c	-AT-GTTGAT-TCAGGCT
224	DK13	4d	-GCT-GT
225	GB809	4e	-ACT-GAA
29	BNL7	4k	-GCATGAT-TCGAAT
31	BNL8		-GCT-GTTGATT-TCGAAC-AT
33	BNL9	4 k	CGCT-GTTGACGAACC
35	BNL10		-GCT-GTTGAT
37	BNL11		-GCGTTGAT
39	BNL12		CCAGGA
39	DIVLIZ	41	CC-AGGACAGGC-I
226	BE95	5a	-ACT-GAAATAGGTC-C-AGGCT
220	ככםם	Ju	A CI C A A MINOO IC C NO CCI
227	HK2	6a	T-G-CGATCAGC-C-TTT
22,	IIICZ	υa	TCAO C C T T
228	FR1	72	-AA-CT-GAGGTTTAGGT-A-TATCA-GTT
220	FKI	/a	-AA-CI-GAGIIIAGGI-A-IA - ICA GII
43	VN4	0 2	-TCCTAGCGCAGGTCATGTCA-GTT
43	A144	oa	-1CC1AGCGCAGG1CAIGICA-GII
47	VN12	0 =	CTGGTGAGAATGT-TGATC
* /	A 14 T T	Ja	C I GGIGADAAIGI-IGAIC
51	NE98	10=	-AT
31	NEJO	IUa	-A1GGGG1-A-GGAGA-A1C-C-AG11



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Fig. 1S

SEQ I	D		
NO			901 950
208	HCV-1	1a	ACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACGGGTCACCG
209	HCV-J	1b	GTAA
210	HC-G9	1c	G-G-AT
3	BNL1	1d	G-AGCA
7	BNL2		AG-AGA
11	FR2	1 f	GTG-ACTTCTCT-TC
	1112		
211	HC-J6	2a	GTAC
212	HC-J8		CAGCTCAATCCCT
213	S83		GTCG-AACTCACGCTA
214	NE92		GTCG-ACCACACCTAT
15	BNL3		GTCG-AA
17	FR4		GTCG-AACACA
		21	T-CG-ATC
19	BNL4		GTCG-AGA
23	BNL5	Zn	G1CG-AGA
			CMC 03.00 M 0 00.0 0 3 0 0 0 M
215	NZL1		GTCGACCTCGC-GCAC-TT-AAT
216	HCV-TR		GTGACGCGACAG-TT-AAT
217	NE48		GTTGCACAC-GCATG-TT-AT
218	NE274	3d	GTGACCAC-GCTTCT-AAA-
219	NE145		GTCGACCCGT-GCA
220	NE125	3f	GTCGTTGAC-ACAACTAAT-A
221	Z4		G-AGTCCA-TCCCA-
222	Z 1		CG-ACCTTCG-CTCA-
223	GB358	4c	G-ACTCCG-GGCG-TCA-
224	DK13	4d	CACTCCA-AACAA-
225	GB809	4e	CG-ACTTCCG-AGTCT
29	BNL7	4k	TATC
31	BNL8	4k	G-CG-AT
33	BNL9	4k	CAC
35	BNL10	4k	CG-ATC
37	BNL11	4k	CG-AATC
39	BNL12	41	GTCACCTC
226	BE95	5a	GTGAACCTCAGTG-TC
227	HK2	6a	GTACCA-ACG-CCA-
228	FR1	7a	CG-ATCNA-CN-TCG-CAA-
4.5	1774	0-	
43	VN4	вa	GTCG-AGTCTCCA-AGCTA
47	VN12	9.5	G-CG-ACCTCG-ACCTG
4/	A 1A T 5	Эd	G-CG-MCC1CG-MCC1G
51	NE98	100	GTCG-ACCTC
21	MEDO	Iva	010 0 AC -C-11-C



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Fig. 1T

SEQ ID		
NO		951 957
208	HCV-1	1a CATGGCA
209		1bT
210		1c AT
11	FR2	1f NNNNNNN
211	HC-J6	2aG
212	HC-J8	2b
213	S83	2cT
214	NE92	2d GG
15	BNL3	2eG
17		2f ANN
17	FR4	21 ANN
215	NZL1	3а АТ
216	HCV-TR	3b TG
217	NE48	3c GT
218	NE274	3d GT
219	NE145	3e
220	NE125	3f TT
220	NE125	31 11
221	Z4	4a GG
222	Z1	4b GC
223	GB358	4c G
224	DK13	4d AT
225	GB809	4e GT
223	GBGGS	100 1
226	BE95	5a G
227	HK2	6a GT
228	FR1	7a G
220	- A	,
43	VN4	8a A
47	VN12	9a GG



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Fig. 2A

SEQ ID			
NO			1 50
229	HCV1	1a	MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR
230	HCV-J	1b	R-T
2	BNL1	1d	XXXXXXXXXXXX
6	BNL2	1d	R-TXX
10	CAM1078	1e	VA-
12	FR2	1f	R-T
231	нсј6	2a	R-T
232	HCJ8	2b	R-T
233	CH610	2c	R-T
234	NE92	2đ	R-T
14	BNL3	2e	R-T
18	FR4	2f	P-
235	HCVTR	3b	LRQTLNVV-
236	DK13	4d	R-TM
237	CAM600	4e	R-TM
238	GB809	4e	L-R-TM
28	BNL7	4k	R-TM
239	BE95	5a	R-TM
240	HK2	6a	LR-TT
42	FR1	7a	LR-TM
44	VN4	8a	LR-TI
46	VN13	8b	LR-T
48	VN12	9a	LR-TM
50	NE98	10a	LR-TXVQV-



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Fig. 2B

SEQ ID)		
NO			51 100
229	HCV1	1a	KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP
230	HCV-J	1b	
2	BNL1	1d	X-XSX-XXX
6	BNL2	1d	DOSD-XXH
10	CAM1078	1e	E
12	FR2	1 f	A
231	нсл6	2a	LL
232	HCJ8	2b	
233	CH610	2c	L
234	NE92	2d	
14	BNL3	2e	L
18	FR4	2f	L
10	F.N.4	21	
235	HCVTR	3b	KQ-HLSRSKKL
236	DK13	4d	QLS
237	CAM600	4e	TS
238	GB809	4e	
28	BNL7	4k	XX
239	BE95	5a	AL
240	HK2	6a	Q-QH
42	FR1	7a	V-Q-TS-G
44	VN4	. 8a	
46	VN13	8b	V-HQT
48	VN12	9a	AV-QNQ
50	NE98	10a	SRTS



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Fig. 2C

SEQ II)		
NO			101 150
229	HCV1	1a	RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA
230	HCV-J	1b	
2	BNL1	1d	N
6	BNL2	1d	
12	FR2	1f	S-T
231	HC-J6	2a	VV
232	HC-J8	2b	T
233	CH610	2c	VV
234	NE92	2d	VVVVV
14	BNL3	2e	XXX-VVX
18	FR4	2f	XVV
235	HCV-TR	3b	VV
241	GB116	4c	VV
236	DK13	4d	VVV
237	CAM600	4e	-XXNXVV
238	GB809	4e	VV
242	G22	4f	VV
243	GB549	4g	VV
244	GB438	4h	VV
28	BNL7	4k	N
239	BE95	5a	NK
240	HK2	6a	HNV-A-
42	FR1	7a	NNVL-GVL-GV-A-
44 46	VN4 VN13	8a 8b	NNXV-X- XNNXXX1E
40	AMTO	an	VMW
48	VN12	9a	D-X-NXV-AE
50	NE98	10a	N



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Fig. 2D

SEQ II)		
NO			151 200
229	HCV1	1a	LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL
230	HCV-J	1b	IEVS-I
2	BNL1	1d	XT-HEAS-V
6	BNL2	1d	TT-HEAS-V
12	FR2	1f	-XXGXXXXXXXXXTE-HST-DG
231	HC-J6	2a	I-T-VAE-K-ISTG
232	HC-J8	2b	VVEISSS
233	CH610	2c	ISVVE-K-TSTS
234	NE92	2d	IK-TSSS
14	BNL3	2e	XVV-XVE-K-TSQA
18	FR4	2f	IK-NSHF
20	BNL4	2 q	VVVK-TSTM
24	BNL5	2ĥ	IVK-TSHS
26	BNL6	2i	IIVVA-RS-S
235	HCV-TR	3b	FCGLEYT-TS
241	GB116	4c	-EAVISTVNYAS-V
236	DK13	4d	LNYS-V
237	CAM600	4e	AVI
238	GB809	4 e	GVNYAS-V
242	G22	4 f	AVI
243	GB549	4q	AVI
244	GB438	4h	AVI
30	BNL7	4k	I-FINYVS-I
32	BNL8	4k	IINYTS-I
34	BNL9	4k	IINYH-TS-I
245	BNL9	4k	IIXXTNYVS-I
36	BNL10	4k	IXTNYVS-I
38	BNL11	41	IQHYVS-I
239	BE95	5a	VPYAS-I
240	нк2	6a	AII
42	FR1	7a	AIIK-AS-I
44	VN4	8a	XXIXXXX-XXXTAHYT-KS
48	VN12	9a	-XAIIXTLNYA-KS
52	NE98	10a	I-FFLT-TAGLEYAS



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Fig. 2E

SEQ II)		201
NO		_	201 250
229	HCV-1	1a	YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD
230	HCV-J	1b	SLL-A-N
2	BNL1	1d	SIMDGM-M-YD-HLM-LL-VKX
6	BNL2	1d	LSIMSGMAN-SMXLL-VK-
12	FR2	1f	S-GK-IXIPLL-A-I
231	HC-J6	2a	-MT-DTWQLQA-VVEKVTIPVS-NVQQ
232	HC-J8	2b	-YAS-NTWQLTVLENDNGTLHIQVNVKH
233	CH610	2c	-MBVS-NI-Q
234	NE92	2d	-MQWQLRVVEEKIIPVS-NI-VSQ
14	BNL3	2e	-MAS-NWOLXVVENSSGRFHIPIS-NI-VSK
18	FR4	2f	-MAA-DWOLRVVE-SRTFT-VS-NVSR
20	BNL4	2q	-MAS-NIWOMOG-VVELOKIPVNVNO
24	BNL5	29 2h	-MB-HQ-QIPVNVSQ
		211 21	
26	BNL6	21	-MSWQLEE-VVEWKD-TIPVNI-VSQ
235	HCVTR	3b	-VLS-GE-VLTTQ-STTVSTV-T
241	GB116	4c	I
236	DK13	4d	K-TSLAQH
237	CAM600	4e	IATENHLTQLSPY
238	GB809	4e	IATDNHLKTOLSPY
242	G22	4 f	LFVHHLTOLL-APY
243	GB549	4g	
244	GB438	4h	DHH-M-LTVIPLVPY
30	BNL7	4k	-YDHHLOLAPY
32	BNL8	4k	DHHLTOLAPY
			I
34	BNL9	4k	
245	BNL9	4k	LAPY
36	BNL10	4k	KHLAPY
38	BNL11	41	KTTLAPI
246	GB724	4x	I
239	BE95	5a	DNLAMTVQILSAPS
240	HK2	6a	LLDAMLLVDDR-TH-VL-IPN
42	FR1	7a	LS-NFETMLIKAELPVSL-VPN
44	VN4	8a	LETLLKXX-QQASL-VPN
48	VN12	9a	LNGMLKTLTKLSASL-VQN
52	NE98	10a	-MS-GG-ILSTIPVSXVKS



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Fig. 2F

SEQ II)		
NO			251 300
229	HCV-1	1a	GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT
230	HCV-J	1b	SSI-T-TIVA-AMSSYE-
2	BNL1	1 d	ASV-TXAIVXX-FM-XAAM-H-
6	BNL2	1d	ANV-TAAIVT-AFRMLYH-
12	FR2	1f	ANA-IDEVVA-VFM-IGTS
231	HC-J6	2a	PGALTOGTMV-MG-M-AA-M-IVOHF
232	HC-J8	2b	RGALTRST-V-MI-MAAVA-MILS-A-MVONF
233	CH610	2.c	PGTLTKGA-V-VI-MVALMIAA-AVIAOTF
234	NE92	2d	PGALTKGTTIIAFIA-M-AS-V-IIOH-KF
14	BNL3	2e	PGALTKGARAV-MV-A-MIAA-A-IVA-KYF
18	FR4	2 f	PGALTRGATI-MIA-MIAA-VAVVQY-TF
20	BNL4	2q	PGALTRGTTI-MVIV-A-MIAA-VVIVOH-NF
24	BNL5	2h	PGALTRG-TTI-AVFA-MS-F-MIQH-IF
26	BNL6	211 21	PGAXTKGTII-AF
26	PNTO	21	FGAXING111-AF
235	HCVTR	3b	LGVTTASI-T-V-MARQAF-AART-
241	GB116	4c	VGA-LESS-VMAVIGM-S-Q
236	DK13	4 d	LNA-LESQ
237	CAM600	4e	AGA-LEPVMAMIGLMQ
238	GB809	4e	VGA-LEPVMAVGLMQ
242	G22	4f	LGA-LESMV-MTGIA-MRL
243	GB549	4 q	VGA-LESMVMAVIGMR
244	GB438	4ĥ	LGA-L-SV-Q-VMAIHGAMVS-Q
30	BNL7	4k	IGA-LESS-VMAVIX-XGLM-S-R
32	BNL8	4k	IGA-LESS-VMAVIGLM-S-R
34	BNL9	4k	IGA-LESS-VMAVIGAM-S-R
245	BNL9	4k	TAA-LESS-VMAVI-XGLM-SXO
36	BNL10	4k	IGA-LESS-V-VMAVIGLM-S-R
38	BNL11	41	LSA-LMSVVMAS
246	GB724	4x	VDA-LESFVMAVGAMQ
239	BE95	5a	LGAVTAPAV-Y-A-G-AAALMYRQ-A-
240	нк2	6a	ASTGFVA-A-VVSILAQ
42	FR1	7a	SSV-IHGFVA-AFM-IIIR-KY-QV
44	VN4	8a	AST-V-GF-K-V-IMA-AFMGLLRM-QV
48	VN12	9a	ASVSIRGV-E-VA-AFMGLRMYEI
52	NE98	10a	PCAATAST-V-MM-XAALXG-SWRH-Q



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Fig. 2G

SEQ ID			
ÑO			301 319
229	HCV-1	1a	TQGCNCSIYPGHITGHRMA
230	HCV-J	1b	V-DVS
2	BNL1	1d	E
6	BNL2	1d	E
12	FR2	1f	V-DSXXX
231	HC-J6	2a	V-D
232	HC-J8	2b	EQ
233	CH610	2c	V-EX
234	NE92	2d	V-D
14	BNL3	2e	V-E
18	FR4	2f	V-EX
20	BNL4	2g	S-D
24	BNL5	2h	V-D
235	HCVTR	3b	V-TVS
241	GB116	4c	DAV
236	DK13	4d	DT
237	CAM600	40 4e	DT
238	GB809	4e	DA
242	G22	4f	ET
242	GB549	4q	DD
243	GB438	49 4h	DV
30	BNL7	4k	D
32	BNL8	4k	A-D
34	BNL9	4k	D
245	BNL9	4k	D
36	BNL10	4k	E
38	BNL11	41	V-D
246	GB724	41 4x	DT
240	GB / 24	4.	D
239	BE95	5a	V-NSV
240	нк2	6a	V-D
42	FR1	7a	DXNXV
4.4	1774	0-	V-E
44	VN4	8a	V-ET
48	VN12	9a	A-DA
52	NE98	10a	V-D



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Fig.3A

- SEQ ID NO. 1 (BNL1, 1d)
 ATGAGCACGAATCCTAAACCTAAAGAAAAACCAAACGTAACACCAACCGCCGCCCTCAKGGSGTN
 NNNNNNCCGGGTGGCGGTCAGATCGTTGGTGGAGGTTTACCTGTTGCCGCGCAGGGGCCCCAGGNNG
 GGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCACAACCTCGTGGCAGGCGACAGCCTATCCCC
 AAGGCTCCGYCGGYCGAGGGCAGGTCCTGGGCTCAGCCCGGGTATCCTTGGCCCCTCTATGGCAAT
 GAGGCTCCGGGTGGGCGGGGNTGGCTCCTGTCCCCCCGGGGTCTCTCGGCCCAATTGGGGCCCC
- SEQ ID NO. 3 (BNL1, 1d)
 GACGGCGTGAACTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTG
 CTGTCCTGCTTGACGGTTCCAACKACCGCTCACGAGGTGCGCAACGCATCCGGGGTGTATCATGTC
 ACCAACGACTGTTCCAACTCGAGCATCATCTATGAGATGGACGGTATGATCATGCACTACCCAGGG
 TGCGTGCCCTGCGTTCGGGAGGATAACCATCTCCGCTGCTGGATGGCGCTCACCCCCACGCTTGCG
 GTCAAAAAYGCTAGTGTCCCCACTRCGGCAATCCGACGTCACGTCGACTTGCTTGTTGGGGGNNCC
 ACGTTCTGTTCCGCTATGTACGTGGGRGACCTTTGCGGGTCTCTTCCTCGCTGGCCAGCTATTC
 ACCTTTTCACCCCGCATGCACCATACAACGCAGGAGTGCAACTGCTCAATC
- SEQ ID NO. 5 (BNL2, 1d)
 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGGACGTC
 AAGNTCCCGGGTGGTGGTCAGATCGTTGGTGGAGGTTTACCTGTTGCCGCGCAGGGGCCCCAGGTTG
 GGTGTGCGCGGACCAGGAAGACTTCCGAGCGGTCGCAGCCTCGTGACAGGCGACAGCCTATTCCT
 AAGGCTCGCCAGTCCGATGGCAGNNCCTGGGCTCAGCCAGGCATCCCTGGCCCCTCTATGGCAAT
 GAGGGCTGCGGATGGCGGGGTGGCTCCTGTCCCCCCCGCGGCTCTCGGCCCAGTTGGGGCCCC
- SEQ ID NO. 7 (BNL2, 1d)
 GACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTAGCTTTT
 CTGTCCTGCTTGACGGTTCCAACTACCGCTCATGAGGTGCGCAACGCATCCGGGGTATATCATCTC
 ACCAATGACTGTTCCAACTCGAGCATCATCTATGAGATGAGTGGTATGATCTTGCACGCCCCAGGG
 TGTGTGCCCTGCGTTCGGGAGAACAACTCTTCTCGTTGCTGGATGCCRCTCACCCCCACGCTTGCG
 GTCAAAGACGCTAATGTCCCTACTGCGGCAATCCGACGCCATGTCGACTTGCTGGTTGGGACAGCC
 GCGTTTCGTTCCGCTATGTACGTGGGGGACCTCTTGCGGATCCGTCTTCCTTGTCGGCCAGCTATTC
 ACCTTTTCACCCCGCTTGTACCATACAACACAGGAGTGCAACTGCTCAATC



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Fig.3B

SEO ID NO. 11 (FR2, 1f) ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGCAACACCAACCGCCGCCCACAGGACGTT AAATTCCCGGGTGGGGGCAGATCGTGGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGGTTG GGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGCGGAAGGC GACAGCCTATCCCCAAGGCTCGCCGACCCGAGGGCAGGTCCTGGGCTCAGCCTGGGTACC CATGGCCCCTCTATGCTAACGAGGGCTGCGGATGGCGGGATGGCTCCTGTCCCCTCGCG GCTCCCGTCCTAGCTGGGGCCCCAATGACCCCCGACGTAGATCACGCAATTTGGGTAAGG TCATCGATACCCTAACGTGTGGCTTCGCCGATCTCATGGGGTACATTCCGCTCGTCGGCGC CCCCCTAGGGGGCGCTTCCAGAACCCTGNCACATGGTGTCCGGGTCCTGGNAGGCGGCGTGATNNN NNNNNNNNAACCTTCCNGGTTGCTCTTTNNCTATCTTCCTCTTGGCNTTACTCTCTTGCCTCAC AGTCCCCACCTCTGCCTATGAGGTGCACAGCACAACCGATGGCTACCATGTCACTAATGACTGTTC CAACGGCAGCATCGTATATGAGGCAAAGGACATCATCCTTCACACGCCTGGGTGNGTGCCCTGCAT ACGGGAAGGCAATATCTCCCGTTGCTGGGTACCGCTCACCCCCACGCTCGCAGCGCGGATCGCGAA CGCTCCCATCGATGAGGTGCGGCGTCACGTCGACCTCCTCGTGGGGGCAGCCGTGTTCTGCTCAGC CATGTACATTGGGGACCTTTGTGGGGGGCGTCTTCCTCGTTGGGCAATTGTTCACCTTCACGTCCCG GCGGCATTGGACGGTGCAGGACTGTAATTGTTCCATTTACTCTGGCCACATAACGGGCCACCGNNN

SEQ ID NO. 13 (ENL3, 2e)
ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACCAACCGCCGCCCACAGGACGTC
AAGTTCCCGGGCGGCGCCACATCGTTGGCGGACTTTACTTGTTGCCGCGCAGGGGCCCCAGATTG
GGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCCAGCCACGTGGAAGGCCCCATCCCT
AAAGATCGGNGNGCCACTGGCAGGTCCTGGGGACGTCCAGGATATCCCTGGCCCCTGTATGGGAAC
GAGGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCCCGAGGCTCTC

SEQ ID NO. 17 (FR4, 2f) ATGAGCACAAATCCTAAACCTCAAAGAAAAACTAAAAGAAACACTAACCGTCGCCCACAGGAC GTTAAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAG GTTGGGTGTGCGCGCCAAGGAAGACTTCTGAACGGTCCCAGCCACGTGGAAGGCGCCAGCCC ATCCCAAAAGATCGGCGCGCCACTGGCAAGTCCTGGGGACGTCCAGGATACCCTTGGCCCCTGT ACGGGAACGAGGGCTCGGCTGGCAGGGTGGCTCCTGTCCCCCGGGGCTCTCGCCCCTCGTG GGGCCCAAACGACCCCCGGCACAGGTCACGCAACTTGGGTAAGGTCATCGATACCCTCACGTG TGGCTTTGSCGACCTCATGGGGTACATACCTGTCGTCGGCGCCCCTGTGGGCGGCGTTGCCAGA GCCCTCGCGCATGGCGTGCGGGTCCTGGAGGACGGGATAAATTATGCAACAGGGAACTTGCCCGGT GTTARGAACAACAGCCACTTCTACATGGCGACTAATGACTGTGCCAATGACAGCATCGTCTGGCAG CTCAGGGACGCGGTGCTCCATGTTCCTGGATGTGTCCCCTGTGAGAGGTCAGGTAATAGGACCTTC TGTTGGACAGCGGTCTCGCCCAACGTGGCTGTGAGCCGACCTGGTGCTCTCACTAGAGGTCTGCGG GCTCACATTGATACCATCGTGATGTCCGCCACCCTCTGCTCTGCCCTATACATAGGGGACCTATGC GGCGCTGTGATGATAGCAGCGCAAGTTGCCGTCGTCTCACCGCAATACCATACTTTTGTCCAGGAA TGCAACTGCTCCATATACCCAGGCCATATCACAGGACATCGAATGGNN



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Fig.3C

SEQ ID NO. 19 (BNL4, 2g)
GACGGGGTAAATTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCTTGTTGGCTCTT
GACGGGGTAAATTATGCAACAGGGAATCTGCCTGGTAAGAACACCAGTACCATGTACATGGCA
ACCAATGACTGTTCCAACAACAGCATCATCTGGCAAATGCAGGGCGGGTGCTTCATGTTCCTGGA
TGTGTCCCGTGTGAGTTGCAGGGCAATAAGTCCCGGTGCTTGATACCGGTCACTCCCAACGTGGCT
GTGAACCAGCCCGGCGCCCTCACTAGGGGCTTGCCGACCACATTGACACCATCGTGATGGTCGCT
ACGCTCTGTTCTGCACTCTACATCGGGGACGTGTGTGCGCGGTGATGATAGCTGCTCAGGTTGTC
ATTGTCTCGCCGCAACATCACAACTTTTCCCAGGATTGCAATTGTTCCATC

SEQ ID NO. 21 (BNL5, 2h)
ATGAGCACAPATCCTAAACCTCAAAGAAAAACCAPAAGAACACTAACCGCCGCCCACAGGACGTT
ATGAGCACAPATCCTAAACCTCAAAGAAAAACCAPAAGAACACTTGTTGCCGCGCAAGGGCCCCCGGTTG
AAGTTCCCGGGCGGTGGCAGAAACCTTCCGAACGGTCCCAGCCACGTGGGAGGCGCCAGCCCATCCCT
GGTGTGCGCGCGCCACGCAAAACCTTCCGAACGGTCCCAGGATACCCTTGGCCCCTGTATGGGAAC
AAAGATCGGCGCTCCACTGGCAAATCCTGGGGACGTCCAGGGTTCCC
GAGGGCCTTGGTTGGGCAGGATGCCTCTTGTCCCCTCGAGGCTCTC

SEQ ID NO. 23 (BNL5, 2h)
GACGGGATAAACTACGCAACAGGGAATCTGCCCGGTTGCTCCTTTTCTATCTTCTTGCTGGCCTTG
GACGGGATAAACTACGCAACAGGGAATCTGCCCGGTTGCTCAAGAACACCAGCACTCTTATATGGTG
CTATCCTGTCTCACTGTGCCGGCGTCCGCTGCTGCAGCTTAAGGATGCTGTGTTCACGTCCCTGGA
ACCAATGATTGCTCAAACAGCAGCATTGTCTGCTGCTGCTGTGACACCCAATGTGGCC
TGTGTTCCATGTGAGAGGCACCAAAATCAGTCTCGCTGCGGACCAATCGTTGACACCATCGTTGCGTCTGCT
GTGAGCCAACCTGGCGCGCTCACCAGGGGTTTGCGGCGCACATTGACACCATCGTTGCGTCTCCAACTTTTTC
ACCGTCTGCTCAGCTTTGTATGTGGGCGACTTCTGCGGCGCACTTGCTCGATA

SEQ ID NO. 25 (BNL6, 2i)
GACGGGATAAACTATGCAACAGGGAACCTGCCTGGTTGCTCCTTTTCTATCTTCTTACTGGCCCTG
GACGGGATAAACTATGCACCGGGCCCTGCCGTGCAAGTTGCGAACCGCAGTGGTTCTTACATGGTG
CTTTCTTGCATCACCGTGCCGGTCTTTGGCAGCTCGAGGAGGCCGTCCTTCACGTCCCTGGA
ACCAATGATTGCTCGGAACAGCACCACCTCCCGCTGCTGGATACCGGTCACCCCTAACATCGCT
TGTGTTCCCTGTGAGTGGAAGGACAACACCTCCCGCTGCTGGATACCGGTCACCCCTAACATCGCT
GTGAGCCAACCTGGCGCGCTTACCAAGGGCCTGCGGACACATATTGACATCATTGTCGCGTCCGCC
ACGTTCTGCCTTGTCTATGTGGG

SEQ ID NO. 27 (BNL7, 4k)
ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCGCCCCATGGACGTT
AAGTTCCCGGGTGGTCGCCAGATCGTTGGCGGAGGTTTACTTGTTGCCGCGCCAGGGGCCCCAGGTTG
AAGTTCCCGGACTCCGAAGACTTCGGAGCGCCCAACCTCGTGGAGACGCCAACCTATCCCC
GGTGTGCGCGCGACTCCGAGGAAGACTTCGGGCCACCCAGGATATCCATGGCCTCTTTACGGTAAT
AAGGCGCGTCGATCCGAGGGAAGGTCCTGGCCCCCCCGCGGTTCTC
GAGGGTTGCGGGTGGCCANNATGGCTCTTGTCCCCCCCGCGGTTCTC

SEQ ID NO. 29 (BNL7, 4k)
GACSGGATCAATTTTGCAACAGGGAACCTCCCCGGTTGCTCCTTTTCTATCTTCCTCTTTGGCACTC
GACSGGATCAATTTTGCAACAGGGAACCTCCCCGGTTGCTCCTTTTCTATCTTCTCTCTTTGCACCTCCCAGGT
CTCTCCTGCCTGACTGTCCCCGCTTCGGCCATCAACTCACATCTTGCACCTCCCAGGT
ACCAATGATTGCCCGAATTCAAGCATAGTGTACGGTGGGGTAGCCCTTACCCCTACCGTCGCA
TGCGTGCCCTGCGTGAGAGAGGGGAATCAGTCACGTTGCTGGACTTGATGGTGGGGGCCGCC
GCGCCATACATCGGCGCCACTTGAGTCTCTACGGAGTCATGTTGCACTTGATCGGTCAGATGTTC
ACTGTTTCTCAGCCCTTTACATCGGGGATTTTTTGTGGYGGCTTGTTCCATC
TCTTTCCGACCAAGGCGCCACTGGACTACTCAAGATTGCAATTGTTCCATC



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Fig.3D

SEQ ID NO. 35 (BNL10, 4k)
GACGGGATCAATTATGCAACAGGGAATATTCCCGGTTGCTCYTTTTCTATCTTCCTTYTGGCACTT
CTCTCGTGTCTGACTGTCCCCGCTTCGGCCACTAACTATCGCAACGTCTCGGGCATCTACCATGTC
ACCAATGACTGCCCGAATTCAAGCATAGTGTATGAGGCCGACCATCACATCTTAGCACTTCCAGGT
TGCGTGCCCTGCGTGAGAGTGGGGAACCAGTCACGCTGCTGGGTGGCCCTTACCCCTACCGTCGCA
GCGCCATACACCGCGGCGCCGCTTGAGTCCCTGCGGAGTCATGTGGATCTGATGGTGGGAGCTGCC
ACTGTTTGTTCAGCCCTTTACATCGGGGAYTTGTGTGGCGGCTTGTTCTTGGTTGGTCAGATGTTC
TCTTTYCAGCCTCGGCGCCACTGGACTACCCAGGATTGCAATTGTTCCATC



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Fig.3E

SEQ ID NO. 43 (VN4, 7c) ATGAGCACACTTCCAAAACCCCAAAGAAAAACCAAAAGAAACACCATCCGCCGCCCACA GGACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGTGGAGTCTACTTGCTGCCGCGCAG GGGCCCGCGCTTGGGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCCAGCCCAGAGG TAGGCGCCAACCAATACCCAAAGTGCGCCACCAAACGGGCCGTACCTGGGCCCAGCCCGG CCGCGGCTCTCGCCCAAATTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAACTTGGG TAAAGTCATCGACACCCTTACTTGCGGGCTTCGCCGACCTCATGGGGTATATCCCTGTCGTAG GCGCTCCGWTGGGAGGCGTCGCGGNGGCCTTGGCGCATGGGGTCANGGNCATCGAGGACGGNGTAA ATTACGCAACAGNGAATCTTCCCGGNNGCTCTNTCTCTATCTTNCTCTTGGCACTTCTCTCGTGCC TTACAACACCAGCCTCCGCGGCGCATTATACCAACAAGTCTGGCCTGTACCATCTCACCAACGACT GCCCCAACAGCAGCATCGTTTATGAGGCGGAGACACTGATTTTGCACTTGCCTGGGTGTGTACCTT GTGTGAAGRTGRACAATCAATCCCGGTGCTGGGTGCAGGCCTCCCCGACCCTGGCAGTGCCGAACG CGTCTACGCCAGTCACCGGGTTCCGCAAACATGTGGACATCATGGTGGGCGCTGCCGCGTTCTGTT CAGCTATGTATGTGGGGGGACCTGTGCGGGGGCCTTTTCCTCGTTGGACAGCTCTTCACGCTCAGGC CTCGGATGCATCAGGTTGTCCAGGAGTGTAACTGTTCCATCTACACAGGGCATATCACTGGACACC GAATGGCA

SEQ ID NO. 47 (VN12, 7d) ATGAGCACACTTCCAAAACCCCAAAGAAAAACCAAAAGAAACACAAACCGTCGCCCAATGCATGTC AAGTTCCCGGGCGGCGGTCAGATCGTTGGTGGAGTCTACTTGTTACCGCGCGCAGGGGCCCACGTTTG AAGGTGCGCCAGAACCAAGGCCGAACCTGGGCTCAGCCTGGGTACCCCTGGCCCCTTTATGGGAAC GAGGGCTGCGGCTGGGCGGGGTGGCTCTTGTCCCCCCGTGGCTCTCGCCCGGACTGGGGNCCCAAT GACCCCGGNGGAGGTCCCGCAACCTGGGTAAGGTCATCG ACACCCTCACTTGCGGCTTCGCCGACCTCATGGAGTACATCCCTGTCGTTGGCGCCCCCCT TGGAGGCGTTGCGGCGGAACTGGNACATGGTGTCAGGGCCATCGAGGACGGCATAAACTATGCAAC AGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCWCTTGGCACTTCTCTCGTGCCTCACCACGCC TGCCTCCGCACTAAACTATGCTAACAAGTCTGGGCTGTATCATCTAACCAATGACTGCCCCAATAG CAGCATTGTGTATGAGGCGAATGGCATGATCCTGCATCTCCCGGGTTGCGTCCCCTGCGTGAAGAC CGGCAACCTGACCAAGTGTTGGCTGTCGGCCTCCCCGACATTGGCGGTGCAGAATGCGTCGGTGTC CGTGGGCGACTTATGCGGTGGGCTCTTTCTCGTTGGGCAGTTGTTCACGTTCAGACCCAGGATGTA TEAGATOGCCCAGGACTGCAACTGTTCCATCTATGCAGGCCACATCACTGGGCACCGGATGGCG

SEO ID NO. 41 (FR1, 9a) ATGAGCACACTTCCAAAACCCCAAAGAAAAACCAAAAGAAATACTAACCGTCGCCCTATGGAC GTCARGTTCCCGGGCGGCCGGCCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGC CCTCGTTTGGGTGTGCGCGCGACGAGAAAGACCTCCGAACGGTCCCAGCCTAGAGGCAGG CGCCAGCCCATACCAAAGGTACGCCAGCCGACAGGCCGTAGCTGGGGTCAACCCGGCTAC CCTTGGCCCCTTTATGGCAACGAGGGCTGCGGATGGGCGGGATGGCTCCTGTCCCCCCGC GGGTCTCGTCCTAATTGGGGCCCCAACGACCCCCGGCGAAGGTCCCGCAACTTGGGTAAG GTCATCGATACCCTTACATNCGGNCTAGCCGACCTCATGGGGTACATCCCTGTCCTAGGAGG GCCGCTTGGCGGCGTTGCGGCTGCCCTGGCGCATGGCGTTAGGGCAATCGAGGACGGGGTCAATTA CGCAACAGGGAATCTTCCTGGTTGCTCCTTTTCTATCTTCCTCTTAGCACTGTTATCGTGCCTCAC TACACCAGCCTCAGCARTTCAAGTCAAGAACGCCTCTGGGATCTACCATCTTACCAATGACTGCTC GAACAACAGCATCGTTTTTGAGGCGGAGACCATGATACTGCATCTTCCAGGTTGTGTCCCATGTAT CAAGGCGGGGAATGAGTCACGATGTTGGCTCCCTGTCTCCCCCACCTTAGCCGTCCCCAACTCATC AGTGCCAATCCACGGGTTTCGCCGACACGTAGACCTCCTCGTTGGGGCAGCGGCATTTTGTTCGGC CATGTACATCGGAGACCTCTGTGGTAGCATAATCTTGGTAGGGCAGCTTTTTACTTTCAGGCCTAA GTACCATCAGGTTACCCAGGATTGTAACTGCTCTATNAACNCTGGCCACGTCACGGGACACAGGAT GGCA



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Fig.3F

SEQ ID NO. 49 (NE98, 10a)
ATGAGCACACTTCCTARACCACARAGARARACCARAGARACACCAACC?CCGGCCACAGGACGTT
ARGTTCCCAGGCGGCGGTCAGATCGTTGGTGGAGTTTACGTGCTACCACGCAGGGGCCCCCAGTTG
GGTGTGCGTGCAGTGCGCAAGACTTCCGAGCGGTCGCAACCTCGCAGTAGGCGCCCAACCCATCCCC
AGGGCGCGCCGAACCGAGGGCAGGTCCTGGGCTCAGCCCGGGTACCCTTGGCCCCTATATGGGAAT
GAGGCCTGCGGGTGGCCAGGGTGCTCCTGTCCCCGCGCGGTCCTC

SEQ ID NO. 53 (BNL1,1d)
CTCGACAGTTACTGAGAATGACATCCGTGTCGAGGAATCAATATACCAATGTTGTGACTTGGCCCC
CGAGGCTCGCAAGGCCATAAAGTCGCTCACCGAGCGGTGTACATCGGGGGCCCYCTAACCAATTC
AAAAGGACAGAACTGCGGCTACCGTCGGTGCCCCCCCAGCGGCGTGCTGACTACCAGCTGCGGCAA
CACCCTGACATGCTACTTGAAAGCCAGAGCGGCCTGTCGAGCTGCAAAGCTCCGGGACTGCACCAT
GCTCGTGTGCGGGGATGACCTTGTCGTTATCTGTGAGAGTGCGGGAGTCGAGGAAGACGCGGCGAA
CCTACGAGCT

SEQ ID NO. 55 (BNL2,1d)
CTCGACAGTTACTGAGAACGACATCCGTACCGAGGRATCAATCTATCAATGTTGTGACTTGGCCCC
YGAGGCCCGCAAGGCCATAAAGTCGCTCACCGAGCGGCTGTACGTCGGGGGCCCCCTAACCAATTC
AAAGGGGCAGAACTGCGGCTATCGTCGGTGTCGCGCTAGCGGCGTGCTGACCACCAGCTGCGGCAA
CACCCTCACATGCTACTTGAAAGCCAGGGCGGCCTGTCGAGCTGCAAAGCTCCAGGACTGCACGAT
GCTCGTGTGCGGAGACGACCTTGTCGTTATCTGTGAGAGCGCGGGAGTCGAGGAGGACGCGGCGAA
CCTACGAGTC

SEQ ID NO. 59 (CAM1078, 1e)

CGTACAGCCTCCAGGACCCCCCTCCCGGAAGAGCCATAGTGGTCTGCGGAACCGGTGAG
TACACCGGAATTGCCAGGACGACCGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGA
GATTTGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTTTGGGTCGCGAAAGGCCTTG
TGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTCCACAGGA
CGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTCTACCGCCCCCACAGGA
CCTCAAGTTCCCGGCGCGCGCAGCCCGGAAGACTTCGGAGCGCCGAACCTCGTGGGAG
CCCTAGATTGCGTGCGCAGCCCGGAAGACTTCGGAGGTCCTGGCCCAGCCCGGGTA
CCCCTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTCCTGGCCCCTCC
CGGCTCCCGTCCTAGTTGGGGTCCTACTGACCCCCGGGTAGGTCACCAACTTTGGGTAA
GGTCATCGATACCCTCACGTGTTGNTTCGCCGACCTCATGGGGTACATACCG



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Fig.3G

SEQ ID NO. 61 (CAM1078, le)

CTCAACGGTCACTGAAGCTGATATCCGAACAGAGGAGTCCATATACCAATGCTGTGACCTGCACCC CGAAGCACGTGTAGCCATCAAGTCTTTGACTGAAAGGCTGTACGTCGGGGGGCCCTTGACCAATTC AAAAGGGGAAACTGCGGCTATCGCAGATGCCGTGCCAGCGGCGTCTTGACAACCAGCTGCGGCAA CACCCTCACCTGCTATATCAAGGCCCTAGCAGCCTGTAGAGCTGCCAAGCTCCAGGACTGCACCAT GCTCGTCTGTGGCGACGACCTGGTCGTGATCTGCGAGAGTGTAGGGACCCAGGAGGATGCGGCGAG CCTGCGAGCC

SEQ ID NO. 63 (FR2, 1f)

NTCAACAGTCACTGAGAGTGATATCCGTACAGAGGAGTCCATCTACCAATGCTGTGATCTAGACCC CGAGGCTCGCAAGGCCATAAGGTCCCTCACAGAGAGGCTTTATATCGGGGGTCCCCTGACAAACTC AAAAGGGCAGAACTGCGGCTACCGCCGATGCCGTGCAAGCGGCGTCCTGACGACTAGCTGCGGCAA CACCCTCACCTGTTACATAAAGGCCAGGGCAGCCTGTCGAGCTGCGAAGCTCCAGGATTGCTCAAT GCTCGTCTGTGGCGACGACCTTGTCGTTATCTGCGAGATCGAGGGGNTCCANGAGGATCCGTCGAN NNNNNNNNN

SEQ ID NO. 65 (FR16,1g)

SEQ ID NO. 67 (FR16,1g)

NNNNNNGTCACTGAGAGTGATATCCGTGTCGAGGARTCAATTTACCAATGCTGTGACCTGGCCCC
CGAGGCTCGCGTAGCCATAAAGTCGCTCACTGACCGCTATATGTCGGGGGCCCTCTCACCAACTC
AAAAGGACAGAACTGCGGCTATCGCCGGTGCCGTGCGAGCGGTGTGCTGACTACTAGCTGCGGTAA
CACCCTCACATGCTACCTGAAAGCCGCCGCGCCTGTCGAGCTGCAAAGCTCCGGGAATGCACAAT
GCTCGTGTGTGGGGGACGACCTCGTCGTTATCTGTGAGAGTGCGGGGGTCCAGGAGGATGCTGCAAG
CCTNNNNNN

SEQ ID NO. 69 (BNL3, 2e)

CTCGACAGTCACAGAGAGATATAAGNACTGAGGAGTCCATATACCAGGCTTGTTCCTTACCCGA GCAGGCCAGAACTGCCATACACTCATTGACTGAGAGACTCTACGTAGGAGGGCCCATGATGAACAG CAAAGGGCAATCCTGCGGATACAGGCATTGCCGCGCCAGCGGAGTGCTCACCACCAGTATGGGGAA TACCATCACGTGCTACATCAAGGCCCTAGCGGCTTGTAAAGCAGCAGGAATAGTGGCCCCCACCAT GCTGGTGTGCGGGGATGACCTAGTTGTCATCTCAGAGAGTCAGGGAGTCGAGGAGCACCAGCAA CCTGANNNNN



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Fig.3H

SEQ ID NO. 71 (FR4, 2f)

CTCAACCGTCACAGAGAGGGATATAAGAACTGAGGAGTCCATATACCTGGCCTGCTCCTTACCCGA GCAGGCCCGGACTGCCATACATTCATTAACTGAGAGACTTTACGTGGGAGGGCCCATGATGAACAG CAAAGGGCAGTCCTGCGGATACAGGCGTTGCCGCGCTAGCGGAGTGCTCACCACCAGTATGGGGAA CACCATCACGTGTTATGTGAAAGCCCTCGCAGCTTGTAAAGCTGCGGGCATTGTTGCCCCCACGAT GCTGGTGTGCGGCGATGACCTGGTTGTCATCTCAGAGAGTCAGGGGGGCTGAGGAGGACGAGCGAAA CCTGAGAGTC

SEQ ID NO. 73 (BNL5, 2h)

CTCAACAGTCGCGGAGAGAGACATCAGGACCGAGGAGTCCATTTACCTTGCCTGCTCCTTACCCGA GCAAGCCCGAACIGCCATACATTCATTGACTGAGAGACTTTACGTAGGAGGGCCCATGATGAACAG CAAGGGACAGTCCTGCGGTTACAGACGITGCCGCGCGCGGAGTGCTCACCACCACCATGGGGAA TACCATCACATGCTATGTGAAGGCATTAGCTGCCTGCAAAGCTGCAGGCATCGTTGCTCCCACGAT GCTGGTTTGTGGCGACGATCTGGTCATCATCTCAGAGAGTCAGGGAACCGAGGAGGATGAGCGGAA CCTGAGAGTC

SEQ ID NO. 75 (FR13, 2k)

CGNACANCCTCCAGGCCCCCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAG TACACCGGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATAAACCCACTCTATGCCCGGC CATTTGGGCGTGCCCCGCAAGACTGCTARCCGAGTAGCGTTGGGTTGCGAAAGGCCTTG TSGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCATCAT GAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACTAACCGCCGCCCACAGGA CGTTAAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTATACTTGTTGCCNTGCAGGGG NCCCAGGINGNGINTATGCGCAACGANGAAGACINCCGAACAGICCCAGCCACGIGGGAG GCGCCAGCCCATCCCGAAAGATCGGNGCACCACTGGCAAGTCCTGGGGACGTCCAGGATA TCCCTGGCCCCTGTATGGGAACGAGGGCCTCGGGTGGGCAGGGTGGCTCCTGTCCCCCCG GGGCTCCCGCCGTCATGGGGCCCCACGGACCCCCGGCATAGGTCGCGCAACTTGGGTAA GGTCATCGATACCCTCACGTNCGGCTTTNCCGACCTCATGGGGTACATTCCCGTCGTTGG CGCCCAGTAGGNGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGG TCTGTCCTGAATTACCGNGCCAGTTTCTGCTGTGGAAATCAAAAACACCAGMAACACATA CATGGTGACTAACGACTGTTCAAACAGYAGCATCACCTGGCAGCTTNNGNNCGCGGTGCT TCACGTTCCTGGATGCGTCCCCTGTGAACGAGGGGCAACAGTTCCCGGTGCTGGATTCC AGTCACGCCCRACGTAKNCGTGAGCCGACCTGGTGCCCTAACCGAGGGTTTGCGATCGCA CATCGACACCATCGTAGCGTCCGCAACATTTTGTTCTGCCCTCTACATAGGGGATGTATG TGGCGCGATAATGATAGCTGCCCAAGTGGTCATCGTCTCGCCGGAGCATCATCACTTTGT CCAGGACTGTAACTGTTCCATCTACCCGGGCCACATAACGGGGCCTCGTATGTNG

SEQ ID NO. 77 (FR13, 2k)

ATCCACAGTCACTGAAAGAGACATCAGAGTTGAAGAGTCCGTTTATCTGTCCTGTTCACTTCCCGA GGAGGCCCGAGCTGCCATACACTCACTAACTGAGAGGCTGTACGTGGGAGGTCCCATGCAGAACAG CAAGGGGCAATCCTGCGGATACAGGCGCTGCCGCGCCAGCGGGGTGCTCACCACTAGCATGGGGAA TACTCTCACATGCTACTTGAAGGCCCAGGCGGCCTGCAGGGCCGCGGCATTGTTGCACCCACAAT GCTGGTGTGTGGCGACGACCTGGTCGTCATCTCAGAGAGTCAGGGGACTGAGAGGGACGAGAACAA CCTGAGACCT



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Fig.3I

SEO ID NO. 79 (FR18, 21)

CTCAACAGTCACGGAGAGGGACATCAGGAATGAGGAGTCCATATTCCTGGCCTGCTCGTTGCCCGA GGAGGCCCGGACTGTCATACATTCGCTCACTGAGAGACTCTACATAGGCGGGCCGATGATGAACAG CAAGGCCAGTCCTGTGGATACAGGCGTTGTCGCGCCAGCGGGGTGTTCACCACTAGCATGGGCAA TACCATCACGTGCTATGTGAAAGCCATGGCAGCTTGCAGAGCTGCCGGGATTGACGCCCCCCACAAT GTTGGTATGTGGCGACCGACCTGGTGGTCATCTCAGAGAGTCAGGGGACCGAGGAGGACGAAA TCTGAGAGTC

SEQ ID NO. 81 (PAK64,3g)

CTCTTGACTCTACTGTCACTGAACAGGATATCAGGGTAGAAGAAATATACCAATGTTGTGACC
TTGAGCCGGAGGCTAGACGGCAATCAAATCGCTCACGGAACGGCTTTACGTTGGAGGTCCCATGT
TCAACAGCAAGGGGCTCAAATGCGGATATCGCCGTTGCCGTGCTAGCGGTGTATTGCCCACTAGCT
ACGGTAATACAATCACCTGCTACATCAAGGCCAGAGCGGCTGCTCGAGCTGCGGGCCTTCAAGACC
CATCATTCCTTGTCTGCGGAGATGATTTGGTGGTAGTGGCTGAGAGTTGCGKCGTTGATGAGGAGG
ATAGGGCAGC

SEQ ID NO. 83 (BNL8,4k)

CTCCACTGTAACCGAAAAGGACATCAGGCCCGAGGAAGAGGTCTATCAGTGTTGTGACCTGGAGCC CGAAGCTCGCAAGGTTATTACCGCCCTCACAGAAAGACTCTACGTGGGCGGCCCCATGCACAACAG CAAGGGAGACCTTTGTGGGTATCGGAGATGCCGCGCAAGCGGCGTCTACACCACCAGCTTCGGAAA CACACTGACGTGCTACCTCAAAGCCTCAGCTGCTATTAGAGCGGCAGGGCTGAGAGACTGCACCAT GCTGGTTTGCGGTGACGACTTGGTCGTCATCGCTGAGAGCGATGGCGTAGAGGAGGATAACCGAGC CCTCCNAGCC

SEO ID NO. 85 (BNL12,41)

SEQ ID NO. 87 (EG81,4m)

SEO ID NO. 89 (VN13,7a)

CTCAACAGTCACAGAGCGCGATGTCCAGACGGAGCATGACATCTACCAGTGCTGTAAGTTGGAGCCCGCAGCACGGACACGACCATCACATCGCTTACTGACCGATTGTACTNCGGTGGTCCCATGTNTAACTCCTAAAGGTCAGGCATGTGGATACCGTAGGTGCAGGGCCAGTGGCGTCTTGACCACCATCCTGGCCAATACCTCGACTTGCTACTTGAAAGCTCAGGCGGCATGCAGAGGCTGCCGGGCTGAAGGACTTTGACATCGTTGGTCTGCCGAGACCACCTTGTCGTTATTTCGGAGAGTTTTGGGGGTCTCGGAGGACCACTAGTGCACTGCCGAGGCCT



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Fig.3J

SEQ ID NO. 91 (VN4,7c)

CTCGACAGTCACCGAGCGCGACATCCRCACCGAGCACGACATCTACCAATGCTGCCAACTTGACCC
GGTGGCACGCAAGGCTATTACATCTCTGACTGAGCGCTGTACTGCGGWGGGCCCATGATGAACTC
CCGTGGTCAATCATGTGGATACCGTAGGTGCCGAGCCAGTGGCGTGCTCACCACGAGCTTEGGCAA
TACCCTAACATGCTATTTGAAAGCACAAGCAGCGTGTAGGGCAGAAAGCTCAAAAACTATGACAT
GTTAGTCTGCGGAGACGATCTAGTCGTTATCGCGGAGAGTGGAGGAGTCTCTGAGGATGTTGACGC
CCTGCCAGCA

SEQ ID NO. 93 (VN12,7d)

CTCCTCCGTCACGGAGCGTGACATCCGCACTGAACACGACATCTATCAGTGCTGCCAATTAGATCC
GGTAGCACGGAAAGCCATTACATCTCTTACTGAGCGGCTGTACTGCGGCGCCCCCATGTACAACTC
TCGAGGTCAGTCATGTGGGTACCGCAGGTGCCGGGCTAGTGGTGTTCTCACCACAAGCTTGGGCAA
CACCATGACATGCTACCTGAAGGCTCAGGCGGCTTGTAGGGCAGGAGCTCAAAAACTTTGACAT
GTTGGTCTGCGGAGACGACCTAGTCGTTATTGCTGAGAGCGGAGGCCCTGAGGATGCCGGGGC
CCTGCGAGGTC

SEQ ID NO. 95 (FR1,9a)

ATCCACAGTCACGGGGCGCGACATACGCACAGACNAGACATTTACCTGTCCTGCCAGCTCGACCC AGAGGCCCGGAAAGCCATAAAGTCTCTCACTGAGAGGCTCTATGTCGGGGGCCCTATGTACAACTC AAAGGGCCAACTCTGTGGTCAACGCCGATGCCGAGCAAGCGGAGTACTCCCCACAAGCATGGGTAA CACCATCACATGCTTCCTGAAGGCAACCGCCGCTTGCCGAGCAGCCGGCTTTACAGATTATGACAT GTTGGTCTGCGGAGACGATTTGGTTGTCGTAACTGAGAGTGCTGGAGTCAACGAGGATATCGCTAA CCTGCGAGCC

SEQ ID NO. 97 (NE98,10a)

SEQ ID NO. 99 (FR14,11a)

SEQ ID NO. 101 (FR15,11a)



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Fig.3K

SEQ ID NO. 103 (FR19,11a)
CGTACAGCCTCCAGGACCCCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACC
GGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATTAACCCACTCTATGCCCGGAGATTTGGGCGTG
CCCCCGCAAGACTGCTAGCCGAGTAGCGTTGGGTTGCGAAAGGCCTTGTGGTACTGCCTGATAGGG
TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACCGAATCCTAAACCTCAAAG
ACAAACCAAAAGAAACACCAACCGCCGCCCCACAGGACGTTTAGTTCCCGGGCGGTGGCCAGATCGT
TGGCGGGGTGTACTTGTTGCCGCGCAGGGGCCCCAACGTTGGCTGCGCGCGACGAGAAAAGACCTC
GGAGCGGTCCCAGCCGCGGGGGGCCCCAACCTATCCCCAAGGTTAGGCGCACCACCGGCCGTT

SEQ ID NO. 105 (FR19,11a)
CTCTACTGTCACAGAGGGATATACGAACAGAGGAATCCATYTATCTGGCTTGTCAATTGCCCGA
AGAGGCCCGGAAGGCCATCAAATCACTGACAGAGAGACTATACGTGGGCGGCCCGATGGAAAACAG
CAAGGGCCAGGCCTGCGGATACAGGCGTTGCCGCCAAGCGGGGTATTCACCACAAGCTTGGGAA
CACCATGACTTGTTACATCAAAGCCAAGGCGCTTGTAAAGCCGCTGGCATTGTTGACCCAGTGAT
GCTCGTGTGCGGCGACGACCTAGTGGTCATCTCAGAAAGCAAGGGGGGTGGAGGAGGACCAACGAGA
CCTACGANTC

SEQ ID NC. 2 (BNL1, 1d)
MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRGRRQPIP
KAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP

SEQ ID NO. 4 (BNL1, 1d)
DGVNYATGNLPGCSFSIFLLALLSCLTVPXTAHEVRNASGVYHVTNDCSNSSIIYEMDGMIMHYPG
CVPCVREDNHLRCWMALTPTLAVKXASVPTXAIRRHVDLLVGXXTFCSAMYVXDLCGSVFLAGQLF
TFSPRMHHTTQECNCSI

SEQ ID NO. 6 (BNL2, 1d)
MSTNPKPQRKTKRNTNRRPQDVKXPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRDRRQPIP
KARQSDGXXWAQPGHPWPLYGNEGCGWAGWLLSPRGSRPSWGP

SEQ ID NO. 8 (BNL2, ld)
DGVNYATGNLPGCSFSIFLLAFLSCLTVPTTÄHEVRNASGVYHLTNDCSNSSIIYEMSGMILHAPG
CVPCVRENNSSRCWMXLTPTLAVKDANVPTAAIRRHVDLLVGTAAFRSAMYVGDLCGSVFLVGQLF
TFSPRLYHTTGECNCSI

SEQ ID NO. 10 (CAM1078, 1e)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP
KERRPEGR

SEQ ID NO. 12 (FR2, 1f)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGCVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGCVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
KARRPEGRSWAQPGYPWPLYANEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKVIDTLTCGFAD
LMGYIPLVGAPLGGASRTLXHGVRVLXGGVXXXXXNLXGCSXXIFLLXLLSCLTVPTSAYEVHSTT
DGYHVTNDCSNGSIVYEAKDIILHTPGXVPCIREGNISRCWVPLTPTLAARIANAPIDEVRHVDL
LVGAAVFCSAMYIGDLCGGVFLVGQLFTFTSRRHWT
VQDCNCSIYSGHITGHXXX

SEQ ID NO. 14 (BNL3, 2e)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
KDRXATGRSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWG

SEQ ID NO. 16 (BNL3, 2e)
TCXXADLMGYXPVVGAPVGGXARALAXGVRVLEDGINYXTGNLPGCSFSIFXLALLSCVTVPVSXV
TCXXADLMGYXPVVGAPVGGXARALAXGVRVLEDGINYXTGNLPGCSFSIFXLALLSCVTVPVSXV
EVKNTSQAYMATNDCSNNSIVWQLXDAVLHVPGCVPCENSSGRFHCWIPISPNIAVSKPGALTKGL
RARIDAVVMSATLCSALYVGDVCGAVMIAAQAFIVAPKRHYFVQECNCSIYPGHITGHRMA



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Fig.3L

SEQ ID NO. 18 (FR4, 2f)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRAPRKTSERSQPRGRRQPIP
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRAPRKTSERSQPRGRRQPIP
KDRRATGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNLGKVIDTLTCGFXD
LMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLSCITVPVSAIQVKNNS
HFYMATNDCANDSIVWQLRDAVLHVPGCVPCERSGNRTFCWTAVSPNVAVSRPGALTRGLRAHIDT
IVMSATLCSALYIGDLCGAVMIAAQVAVVSPQYHTFVQECNCSIYPGHITGHRMX

SEQ ID NO. 20 (BNL4, 2g)
DGVNYATGNLPGCSFSIFLLALLSCVTVPVSAVQVKNTSTMYMATNDCSNNSIIWQMQGAVLHVPG
CVPCELQGNKSRCWIPVTPNVAVNQPGALTRGLRTHIDTIVMVATLCSALYIGDVCGAVMIAAQVV
IVSPQHHNFSQDCNCSI

SEQ ID NO. 22 (BNL5, 2h)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGRSLAEYTCARRGKLRRSSMG

SEQ ID NO. 24 (BNL5, 2h)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAVQVKNTSHSYMVTNDCSNSSIVWQLKDAVLHVPG
CVPCERHQNQSRCWIPVTPNVAVSQPGALTRGLRTHIDTIVASATVCSALYVGDFCGAVMLVSQFF
MISPQHHIFVQDCNCSI

SEQ ID NO. 26 (BNL6, 21)
DGINYATGNLPGCSFSIFLLALLSCITVPVSAVQVANRSGSYMVTNDCSNSSIVWQLEEAVLHVPG
CVPCEWKDNTSRCWIPVTPNIAVSQPGAXTKGLRTHIDIIVASATFCSALYV

SEQ ID NO. 28 (BNL7, 4k)
MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
KARRSEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPSWGPNDPRRSR

SEQ ID NO. 30 (BNL7, 4k)
DGINFATGNLPGCSFSIFLLALLSCLTVPASAINYRNVSGIYYVTNDCPNSSIVYEADHHILHLPG
CVPCVREGNÇSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDXCXGLFLVGQMF
SFRPRRHWTTQDCNCSI

SEQ ID NO. 32 (BNL8, 4k)
DGINYATGNLPGCSFSIFILALLSCLTVPASAINYRNTSGIYHVTNDCPNSSIVYEADHHILHLPG
CVFCVRTGNQSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDLCGGLFLVGQMF
SFRPRRHWTAQDCNCSI

SEQ ID NO. 34 (BNL9, 4k)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAINYHNTSGIYHITNDCPNSSIVYEADHHILHLPG
CVPCVRVGNQSSCWVALTPTIAAPYIGAPLESIRSHVDLMVGAATVCSALYIGDLCGGAFLVGQMF
SFRPRRHWTTQDCNCSI

SEC ID NO. 36 (BNL10, 4k)
DGINYATGNIPGCXFSIFLXALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVYEADHHILALPG
CVPCVRVGNQSRCWVALTPTVAAPYTAAPLESLRSHVDLMVGAATVCSALYIGXLCGGLFLVGQMF
SXQPRRHWTTQDCNCSI

SEQ ID NO. 38 (BNL11, 4k)
DGINYATGXLPGCSFSIFLLALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVFEADHHILHLPG
CVPCVKEGNHSRCWVALTPTVAAPYIGAPLESLRSHVDVMVGAATVCSALYIGDLCGGLFLVGQMF
SFRPRRHWTTQECNCSI

SEQ ID NO. 40 (BNL12, 41)
DGINYATGNLPGCSFSIFILALLSCLTVPASAQHYRNVSGIYHVTNDCPNSSIVYESDHHILHLPG
CVPCVKTGNTSRCWVALTPTVAAPILSAPLMSVRRHVDLMVGAATLSSALYVGDLCGGAFLVGQMF
TFQPRRHWTVQDCNCSI



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Fig.3M

SEO ID NO. 46 (VN13, 7a)

MSTLPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPXGSRPNWGPNDPRXRSRNLGKVIDTLTXXFAD

SEC ID NO. 44 (VN4, 7c)

MSTLPKPQRKTKRNTIRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRSRNLGKVIDTLTCGFAD LMGYIPVVGAPXGGVAXALAHGVXXIEDXVNYATXNLPXXSXSIXLLALLSCLTTPASAAHYTNKS GLYHLTNDCPNSSIVYEAETLILHLPGCVPCVKXXNQSRCWVQASPTLAVPNASTPVTGFRKHVDI MVGAAAFCSAMYVGDLCGGIFLVGQLFTLRPRMHQVVQECNCSIYTGHITGHRMA

SEQ ID NO. 48 (VN12, 7d)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQARGRRQPIP KVRQNQGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPDWXPNDPRXRSRNLGKVIDTLTCGFAD LMEYIPVVGAPLGGVAAELXHGVRAIEDGINYATGNLPGCSFSIFXLALLSCLTTPASALNYANKS GLYHLTNDCPNSSIVYEANGMILHLPGCVPCVKTGNLTKCWLSASPTLAVQNASVSIRGVREHVDL LVGŁAAFCSAMYVGDLCGGLFLVGQLFTFRPRMYEIAQDCNCSIYAGHITGHRMA

SEQ ID NO. 42 (FR1, 9a)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRQPTGRSWGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRSRNLGKVIDTLTXXLAD LMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLALLSCLTTPASAIQVKNAS GIYHLTNDCSNNSIVFEAETMILHLPGCVPCIKAGNESRCWLPVSPTLAVPNSSVPIHGFRRHVDL LVGAAAFCSAMYIGDLCGSIILVGQLFTFRPKYHQVTQDCNCSXNXGHVTGHRMA

SEQ ID NO. 50 (NE98, 10a)

MSTLPKPQRKTKRNTNXRPQDVKFPGGGQIVGGVYVLPRRGPQLGVRAVRKTSERSQPRSRRQPIPRARRTEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRR

SEO ID NO. 52 (NE98, 10a)

DGINFATGNLPGCSFSIFLLALFSCLLTPTAGLEYRNASGLYMVTNDCSNGSIVYEAGDIILHLPG CVPCVRSGNTSRCWIPVSXTVAVKSPCAATASLRTHVDMMVXAATLCSALYVGDLCGALFLXGQGF SWRHROHWTVODCNCSI

SEQ ID NO. 54 (BNL1,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERIYIGGXLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLROCTMLVCGDDLVVICESAGVEEDAANLRA

SEQ ID NO. 56 (BNL2,1d)

STVTENDIRTEXSIYQCCDLAXEARKAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLQDCTMLVCGDDLVVICESAGVEEDAANLRV

SEO ID NO. 58 (FR17,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARACRAAKLQDCTMLVCGDDLVVICESXGVEEDAANLRV



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Fig.3N

SEO ID NO. 60 (CAM1078, le)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP KERRPEGRSWAQPGYPWPLYGNEGCGWAGXLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCXFAD LMGYIP

SEQ ID NO. 62 (CAM1078,1e)

STVTEADIRTEESIYQCCDLHPEARVAIKSLTERLYVGGPLTNSKGENCGYRRCRASGVLTTSCGN TLTCYIKALAACRAAKLQDCTMLVCGDDLVVICESVGTQEDAASLRA

SEQ ID NO. 64 (FR2, 1f)

STVTESDIRTEESIYQCCDLDPEARKAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYIKARAACRAAKLQDCSMLVCGDDLVVICEIEGXXEDPSXXXX

SEQ ID NO. 66 (FR16,1g)

MSTNPKPQRKTKRNINRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KARRSEGRSWAQPGYPWPLYGNEGMGWAGWLLSPHGSRPSWGPSDPRRRSRNLGKVIDTLTCGFAD LMGYIPLVGAPLGGVARALAQGFRDL

SEQ ID NO. 68 (FR16,1g)

XXVTESDIRVEXSIYQCCDLAPEARVAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKAAAACRAAKLRECTMLVCGDDLVVICESAGVQEDAASXXX

SEQ ID NO. 70 (BNL3, 2e)

STVTERDIXTEESIYQACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRHCRASGVLTTSMGN TITCYIKALAACKAAGIVAPTMLVCGDDLVVISESQGVEEDDRNLXX

SEO ID NO. 72 (FR4, 2f)

STVTERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVVISESQGAEEDERNLRV

SEQ ID NO. 74 (BNL5, 2h)

STVAERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVIISESQGTEEDERNLRV

SEQ ID NO. 76 (FR13,2k)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLXCRXPRXXXCATXKTXEQSQPRGRRQPIP KDRXTTGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHRSRNLGKVIDTLTXGFXD LMGYIPVVGAPVXGVARALAHGVRVLEDGINYETGNLPGCSFSISLLALLSITXPVSAVEIKNTXN TYMVTNDCSNXSITWQLXXAVLHVPGCVPCEREGNSSRCWIPVTPXVXVSRPGALTEGLRSHIDTI VASATFCSALYIGDVCGAIMIAAQVVIVSPEHHHFVQDCNCSIYPGHITGPRMX

SEQ ID NO. 78 (FR13,2k)

STVTERDIRVEESVYLSCSLPEEARAAIHSLTERLYVGGPMQNSKGQSCGYRRCRASGVLTTSMGN TLTCYLKAQAACRAAGIVAPTMLVCGDDLVVISESQGTERDENNLRP



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Fig.30

SEQ ID NO. 80 (FR18,21)

STVTERDIRNEESIFLACSLPEEARTVIHSLTERLYIGGPMMNSKGQSCGYRRCRASGVFTTSMGN TITCYVKAMAACRAAGIDAPTMLVCGDDLVVISESQGTEEDFRNLRV

SEQ ID NO. 82 (PAK64,3g)

STVTEQDIRVEEEIYQCCDLEPEARRAIKSLTERLYVGGPMFNSKGLKCGYRRCRASGVLPTSYGN TITCYIKARAARAAGLQDPSFLVCGDDLVVVAESCXVDEEDRAALR

SEQ ID NO. 84 (BNL8, 4k)

STVTEKDIRPEEEVYQCCDLEPEARKVITALTERLYVGGPMHNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKASAAIRAAGLRDCTMLVCGDDLVVIAESDGVEEDNRALXA

SEQ ID NO. 86 (BNL12,41)

STVTEKDIRVEEEIYQCCDLXPEARKAISALTEXLYLGGPMYNSKGELCGYRRCRASGVYTTSFGN TVTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESEGVEEDSQPLRA

SEQ ID NO. 88 (EG81, 4m)

STVTERDIRVEEEVYQCCDLEPEARKAISALTERLYVGGPMFNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESDGVDEDRRALQA

SEO ID NO. 90 (VN13,7a)

STVTERDVQTEHDIYQCCKLEPAARTAITSLTDRLYXGGPMXNSKGQACGYRRCRASGVLTTILAN TLTCYLKAQAACRAAGLKDFDMLVCGDDLVVISESLGVSEDTSALRA

SEQ ID NO. 92 (VN4,7c)

STVTERDIXTEHDIYQCCQLDPVARKAITSLTERLYCXGPMMNSRGQSCGYRRCRASGVLTTSLGN TLTCYLKAQAACRAAKLKNYDMLVCGDDLVVIAESGGVSEDVDALRA

SEQ ID NO. 94 (VN12,7d)

SSVTERDIRTEHDIYQCCQLDPVARKAITSLTERLYCGGPMYNSRGQSCGYRRCRASGVFTTSLGN TMTCYLKAQAACRAXKLKNFDMLVCGDDLVVLAESGGVPEDAGALRV

SEQ ID NO. 96 (FR1,9a)

STVTGRDIRTEXDIYLSCOLDPEARKAIKSLTERLYVGGPMYNSKGOLCGORRCRASGVLPTSMGN TITCFLKATAACRAAGFTDYDMLVCGDDLVVVTESAGVNEDIANLRA

SEQ ID NO. 98 (NE98, 10a)

STVTEQDIRVELSIFQACDLKDEARRVITSLTERLYCGGPMFNSKGQHCGYRRCRASGVLPTSFGN TITCYIKAKAATKAAGIKNPSFLVCGDDLVVIAESAGIDEDKSALRA

SEQ ID NO. 100 (FR14,11a)

STVTERDIRTEESIYLSCQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRV



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Fig.3P

Figure 3 - continued

SEQ ID NO. 102 (FR15,11a)

 ${\tt STVTERDIRTEESIXXACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGNTMTCYIKAXAACKXAGIVDPVMLVCGDDLVVISESKGVEEDQRDLXX}$

SEQ ID NO. 104 (FR19,11a)

 ${\tt MSINPKPQRQTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRVGVRATRKTSERSQPRGRRQPIPKVRRTTGR}$

SEQ ID NO. 106 (FR19,11a)

STVTERDIRTEESXYLACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRX



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4B
Fig.

Core-V	KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLS	SRTS
SEQ ID	00	104
Type	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	10a 11a
Isolate	J 000 00 9 ONEEZP 4	



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	RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAR		N	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	X	L-SN	NSH	1VVV	2THRI,	3	4	SEQ ID NO: 16XXX-VVX	\n-\n\n\n\n\n	\-X\\XXXHH	5VV	1	^^^	\n-\n-\n-\n-\n-\n-\n-\n-\n-\n-\n-\n-\	\n	2	3	^^-^-^-	N	NI-B	ì	×	i	i	NNVL-GV-A-	
SEQ	22	230	7	9	10	12	99	23	23	23	234	14	18	9/	23	24	23	23	23	24	24	24,	28	23	24	46	44	48	42	C C
Туре	1a	1 b	1q	1d	16	14	19	2a	2p	2c	2d	2e	2£	۲ <u>۲</u>	39	4°C	4q	4e	4e	4 £	49	4h	4 k	5 a	6 a	7a	7c	7d	9a	109
Isolate	HCV1	HCV-J	BNL1	BNL2	CAM1078	FR2	FR16	HC-J6	HC-J8	CH610	NE92	BNL3	FR4	FR13	HCV-TR	GB116	DK13	CAM600	GB809	G22	GB549	GB438	BNL7	BE95	HK2	VN13	VN4	VN12	FR1	NE98



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Isolate HCV1	Type 1a	SE ID 22	V1 200 LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL
HCV-J BNL1	ag g		- XI-HEAS-V
FR2	1 1 1 1	12	
FR16	19	99	
HC-J6	2a	231	AE-K-
HC-J8	5 5 7	232	SEST I I I I SEST I I I I I
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E92	2d	234	SSSL-XID-AIIII
BNL3	2e	16	XIXXXV-XVE-K-TSQA
FR4	2£	18	IK-NSHF
BNL4	2g	20	MLST-XVV
NL5	2h	24	SHSL-Y\
BNL6	2i	26	I
FR13	2k	9/	IESS/I-X-VVEIK-TXNT
BR36	3a	255	TEM
HCV-TR	3p	235	A-G
24	4g	226	EHYAS-I
GB809-4	4a	257	EHYAS-I
Z1 211.0	4p	258	E
3116 2116	4, 4	4.7	\-\S\-\Z\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
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DK13	4 4 0 4	236	N-SAN
CAM600	4 6	237	- 1
GB809-2	4 e	238	AVI
CAMG22	4£	261	I-SLI-NAV
CAMG27	4 £	262	I-ST-HYHV
GB549	49	243	AVI
GB438	4 h	244	AVIQHYAS-I
NL7	4 k	30	I-FINYVS-I
BNL8	4 k	32	I-SLXNI
BNL9	4 7	34	I-SL-HANI
ML10	4 k	36	I-SAANLXXII



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I - SA	I-SRADX	VPYAS-I	AIII	XXIXXXXX-X-XXTAHYT-KS	-XAIIXXTLNYA-KS	I-K-AIIK-AS-I	T-FBT-TAGI.RVBS
38 40	239	263	240	44	48	42	7,
44 41						9a	
BNL11 BNL12	BE95	BE100	HK2	VN4	VN12	FR1	NE98



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V4 250 YTRD A-N	VKX	-A-I	VKH	0-1-0	OSA.	VSK	-VSR	OSA-	NSQ.	VSR	VKY	V-T	VAH	AVS	APY	-APY	APY	APY	AQH	SPY	SPY	-L-APY	L-APH	APY	-VPY	-APY	-APY	-APY	-APY	-APY
V3 CVREGNASRCWVAMTPTVATRD	1 1	-IIPLL-A-I	-EKVTIPVS-NVQQ -ENDNGTLHIQVNVKH	-EQIPVS-NI-Q	H	1	1	ONA N AAT N OTA - OSA N AAT O - OH - A -	1 1 1	1	QDT-T-TPV	-STTVST-	TPV	TPV	TPL	!	N	VQL	K-TSL	OI			1	TPL	TVIPL		TQL	-SI	-0ō-	KHL
V1 V3 V4 201 XHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD	- I	S-G	X-N	SWQLEG-V	0	N-S	0-A	8	S	OMTX-S	S	S-G	1 1 1 1 1 1 1 1	A	TTEHH-M-L	LLLLL-		TEHHLL-	LTDYHL	A	A	¥	4 - EI	1 1 1 1 1 1 1 1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TDHH	IDHHI	DHH	LFDHHL
	- 1-1	,						- W-			5 -VL-		I 99	I L	8	7 1	69		236	1	1		I 2	43	4 :	-X- (; -:	`;	į	<u>;</u>
Type SEQ ID ID 230	•	Н (2b 23;		2d 234			29 20 2h 24				3b 23									4e 238			49 24	7	m	ო	4k 34	m	4k 38
Isolate HCV-1 HCV-J	BNL1 BNL2	FR2	HC-08	CH610	NE92	BNL3	FR4	BNL5	BNL6	FR13	BR36	HCV-TR	24	GB809-4	21	GB116	GB215	GB358	DK13	CAM600	GB809-2	CAMGZZ	CAMG27	GB549	GB438	BNL7	BNL8	BNL9	BNL10	BNL11



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BNL12	41	40	L
GB724	4×	246	ITDHHLAVS
BE95	Sa	239	OILSAPS
BE100	5a	263	QILSAPS
HK2	6a		LLDAMLLVDDR-TH-VL-IPN
VN4	7c		LQASL-VPN
VN12	7d		LNGMLKTLTKLSASL-VQN
FR1	9a	9a 42	LS-NFETMLIKAELPVSL-VPN
NEGR	100		-MS-GTS-111

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Isolate

$\frac{V4}{251}$	PATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT	VAAA	W	W-I-	1 1 1 1 1 1	T-V-MI-MAAV	PGTLTKGA-V-VI-MALMIAA-AVIAQTF	PGALTKGAII-MVVALM-AA-VVVVQH-TF	PGALTKGTTIIAFIA-M-AS-V-IIQH-KF	AR	-A	-TTI-MVIVA-MIAA-VVIV	PGALTRGTTI-AVFA-MS-F-MIQH-IF	PGAXTKGTII-AF	PGALTEGSTI-AFIVAIMIAA-VVIVEH-HF	VGATTASI-S-VAMMAARQ-	LGVTTASI-T-V-MARQAF-AAT-	PGA-LESFV-MAGAMMIR	1 1 1 1	PNA-LESMVMAMF-IGD-R	BI	IGA-VESFV-MMAVIGM-S-R	IGA-LESS-VMAAIGM-S-Q	LNA-LESVMGIVGQ	VMAMI	VMAV	LGA-LESMVMTGIAMRL	IGA-LESMVMTIGIM-N-RL	VGA-LESMV-M-AVIGMR	I	S-VMAVIX-XGL	S-VMAVIGL	-S-VMAVIGA	TAA-LESS-VMAVI-XGLM-SXQ	-MDTNWN-00
ΠD	229	1 4.	œ	12	231	232	233	254	234	16	18	20	24	56	9/	255	235	256	257	258	241	259	260	236	237	238	261	262	243	244	30	32	34	36	0
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	HCV-1	BNL1	BNL2	FR2	HC-J6	HC-J8	CH610	S83	NE92	BNL3	FR4	BNL4	BNL5	BNL6	FR13	BR36	HCV-TR	24	GB809-4	21	GB116	GB215	GB358	DK13	CAM600	GB809-2	CAMG22	CAMG27	GB549	GB438	BNL7	BNL8	BNL9	BNL10	TTTNIG



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0	YRQ-A-	YRQ-A-	LRM-QV	RMYEI	R-KY-QV	-SWRH-Q
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LSA-LMSVVMAS	LGAVTAPAV-Y-A-G-AAALMYRQ-A-	2-G-AAAL-AL	AST-V-GF-K-V-IMA-AFMGLLRM-QV	ASVSIRGV-E-VR-AFMGLRMYEI	SSV-IHGFVA-AFM-IIIR-KY-QV	PCAATAST-V-MM-XAALXG-SWRH-Q
SV V M	9AV-Y-	7AV-Y-77	3F-K-V-IM	3V-E-V	3FV	3T-V-MM
LSA-LMS VDA-LES	LGAVTA	AST-TA	AST-V-(ASVSIR	SSV-IHC	PCAATAS
41 40 4x 246	239	263	4.4	48	42	52
41 4x	5a	d d	70	7d	9a	10a
BNL12 GB724	BE95	BEIOU	VN4	VN12	FR1	NE98

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V5 203	TOGENCSIYPGHITGHRMA V-DVS	-D	4	V-D		
SEQ ID	222 230 4	12 231 232 233	$0 \times 0 \times 0 \times 4$	യയയയ	22222 2222 236 236 236	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Type	13 13 13 13	1f 2a 2b	22 Fe d C	22 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Isolate	HCV-1 HCV-J BNL1 BNL2	FR2 HC-J6 HC-J8 CH610	S83 NE92 BNL3 FR4 BNL4 BNL5	FR13 BR36 HCV-TR Z4 GB809-4	116 116 116 116 116 116 116 116 116 116	CAMG22 CAMG27 CAMG27 GB549 GB438 BNL7 BNL8 BNL9 BNL9 BNL10 BNL11



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- :	-N-	-D	V-DTV	-E	-DA	DXNX	V-D
246	239	263	240	44	48	42	25
4x	5a	5a	6а	7C	7d	9a	10a
GB724	BE95	BE100	HK2	VN4	VN12	FR1	NE98



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7932	CTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAAT	5AT'T'T'	GTATGTCATA	GTA	GTATGTCAT	AGAGCTTAAT-CA	NATTTT	NNNNNNNTTTTTRTT	ACAA-GTT-CAT-GGG	ACGGAA-AAAAT-CATGG	G	ACAGTAA-ATT-CATGG	AG-GA-GCT-CT-G	AT-CG-TT-TG-	A	ATACAGA-GGTAAGA	TTACATA-GAGA	TTACAGTA-GGTAAA-AA-
	264	265 266	53	22	57	61	63	29	267	268	69	71	73	77	79	269	270	81
Type	1a 1	9 9	1d	1q	1q	1e	1£	1g	2a	2 p	2e	2£	2h	2k	21	3 a	3p	39
Isolate	HCV-1	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	Т9	PAK64

Fig. 5A NS5B nucleotide alignment

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	TACA-AGA-GGTCAGGTG	TACA-AGA-GGTCAGG-ATG- TACA-AAA-GGTCAGG-ATG-	A-GGTC	TGTG-	TACA-BGA-GC-CA-BGTG-	GGA-AGA-GGTCA-AGT	CACAGA-GGTCAGGTG-	GCTCACATAATGTAT-TT	AACTGAGC-T-ACG-	3CC	T-CGC-TCTAC-C-ACTG-	AG-G-CACA-ACNA-ACTTG-	TCAGA-GGTAACTTT-CTTGG	TCAGAGAAAT-CT-TG-	TAAGAAAT-CYYTGG	TTAGTAAAAT-CYT-TGG
7932	1	 	1 1 1	1	1	1		-9	A-		L	A	1	-L	1 1 1	
SEQ ID	271	272 273	274	275	83.0	85	87	277	89	91	93	95	97	66	101	105
Туре	4c	4 4 0 0	4c	4. o 6	4 ק אַע	41	4m	5a	7a	7c	7d	9a	10a	11a	11a	11a
Isolate	GB48	GB116 GB215	GB358	GB809	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19



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	GACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCCCTCACCGAG	T-G-CG-GA-ACAAA	- 1	-AAAG	-AAA-GA	AAT	-ACTAC-CAGT	AACT-TAC-CGT	AACTAC-CAT-GT	GACTAC-TAT-AT	AACTAC-TAT-GT		GACT-TAC-TGT	GAGA-TGTCCG	GAAGGCG-TA	TGGG-GTA-ACGAAGG
7982	[-1 1	T-G-CG-GA-ACA	T-G-CYG-GAA		-CTAG-GTAA	-CG-CG-GTAAG-CT	CTC-T-GCC-GAGG-GA-ACTAC-CAGT	CTCTGCCT-AAGA-AACT-TAC-CGT	CTC-T-ACC-GAGGA-F	CCCTC-T-ACC-GAGGG	CCCTC-T-ACC-GAGAACT	CCTCATCC-GAGG-GA-CT	CCCTCGT-GCC-GAGG-GGACT-TAC-TGT	-CATAGG-GA-GAGA-TGTCC	-C	TGG-GTA-
SEQID	264	266	22.	61	63	67	267	268	69	71	73	77	79	269	270	81
Type	1a 1b	19 P	19 ;	j e	1.£	1g	2a	5 p	2e	2£	2h	2k	21	3a	3p	3g
Isolate	HCV-1 HCV-J	BE90	BNL2	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64



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	8031		:	!		;	-A	-A	;	!	-A	ပု	:	;	-	-	-		
		AAAT-CCGAA-	AGAAT-CCGAA-	i	-AT-CTG	-AATAAGCCGG	TGATCCGAGA	TTA	4AATCCGA-	AATCCGG-	AACGC	A	TT-CATGT-	1	1TTT-	TGA-CTAG-	AAGGA-	TAAAA-	•
		AA	1	l l		AA-	AA	TAA-	AAZ	AA	GT	AGACF	AAA-	AGAA	GAAZ	TA-GAG-	GAAA	GAA-	5
	7982		B-BBB	BB	B-BB	9-9BBL	-CCGGAATGATCCG	BB	AAAAG	TGGAG-G	CA-TGTT-GC-GTG-G	-CB-GT-GGGC	-CCC-ATGGTG	-CCC-AT-ATGGTAGAAAT-CATTT	CCCC-GAG-G	CCA-GGA-G-G-G	CC-AT-GCCTGAAG-G	CC-AT-GCC-GAAG-G	נ ניייי ניייי דיייי
SEQ		271	272	273	274	275	276	83	82	87	277	83	91	93	95	97	66	101	207
Type		4c	4°C	4c	4c	4 e	49	4 4 4	41	4 m	Sa	7a	7c	7d	9a	10a	11a	11a	נו
Isolate		GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	0103

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2E
Fig.

α	ACTGCG	-TAT	D	CAAC	-ACAAC	CAAAC	ACGAGCA-GTTCAGC-ACCC	-ACAGC-AAC-ATC	TGCAGC-AAC-ATC	TGCAGC-AACTC	TGCAGC-AACTC	'AGCAGC-AC-ATC	TGCAGC-AACCTCT	'TCAGC-ACCC-AT	'ACAGT-ACTCC-G	'TCAGC-ACTCA
2508	AGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGA				A-CA-C	CAC			ACCAAGCA-G-TGCAGC-AAC-ATC	ACGAGCA-G-TGCAGC-AACTC	ACAAGCA-G-TGCAGC-AACTC	GCGATCA-GCAGCAGC-AC-ATC	ACCA-ACGGA-G-TGCAGC-AACCTCT-	Ī) CGCA-CATCA-GTACAGT-A	CCATCA-GTTCAGC-ACTCA
e SEQ ID	264	26.0	20.0	57	63	67	267	268	69	71	73	77	79	269	270	81
Type	1a	199	1 g	19 19 19	1 £	19	2a	2 p	2e	2£	2h	2k	21	3а	3b	39
Isolate	HCV-1	BE90	BNL2	FR17 CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64



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	-CCGCTCA-GCATCAGC-AACCTG	ACCCCCCCCCCACCIG	ACGCTCA-GCATCAGC-AACCTGT ACCGCCA-GCATCAGC-AACCTT	ACCGCTCA-GTACC-ACCTA	ACCGCCA-GCACAGC-AA	RCCT-GCCA-GTATCAGC-AACT	ACGCTCA-GTTTCAGC-AACCTAT	C-CGCTGACA-GTATCAGC-AC-AC-AT	C-AT-GCINCTTCA-GINTCT-AATCGCAT	CGCTGCWGCA-G-TGCCC-TTC-ATCAT	CGCTGCCCA-GTACTC-ATCTCAT	CCCA-GTACACC-ACTT	CCTGTTA-GTTCAGC-AAC-AC	AACGCGA-GGAACAGC-ACCGCT	AACGCGA-GGAACAGC-AACCGC	AACGCGA-GGAACAGC-ACCGC
SEQ ID	271	273	274 275	276	83	82	87	277	89	91	93	95	97	66	101	105
Туре	7 t	7 4 4	4 4 0	49	4 k	4]	4m	5 a	7a	7c	7d	9a	10a	11a	11a	11a
Isolate	GB48	GB215	GB358 GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19

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Isolate	Туре	SEQ ID	
			8082
HCV-1	la	264	CTATCGCAGGTGCCGCGCGGCGTACTGACAACTAGCTGTGGTAAC
HCV-J	1p	265	TCC
BE90	1b	266	C-AG-
BNL1	1q	53	CD
BNL2	1g	52	-IIG
FR17	1q	57	CICICI-
CAM1078	1e	61	TC
FR2	1£	63	CC-ATACG
FR16	1 <u>g</u>	67	CCTTGT
HC-J6	2a	267	GCA-GC-T
HC-J8	5 p		CA-GC-TATTT-CCCATGGT
BNL3	2е		ACA-GCATAGCCCTATGGT
FR4	2£	71	ACA-GC-TTAGCCC-TATGG
BNL5	2h	73	TCA-AC-T
FR13	2k	77	ACA-GC-C
FR18	21		ACA-GC-TTCGGT-CCATGCT
T1	3а	269	TCTCTCTACC-TCTCC
T9	3p	270	C

HCV-1 HCV-J BE90 BNL1 BNL2 FR17 CAM1078 FR2 FR2 HC-J6 HC-J6 HC-J8 BNL3 FR4 BNL3 FR4 FR4 T1 T1

Fig. 5G

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2H
Fig.

8131	ACTACCCTCG	-TCTACC	AACTACCCTCG	AACTACCCTCG	'5 GTATACCCTCG	BCCTACCCTCG	ATCA		A	ATATGCCT-CCTATGC	A-GCTCTC-C-T-CTG-CCT-	ACTGCCGTGCT-	GTTTCT-CCATGC	AAAACC-CAATG	CTTTGGAC-CCTCG	TTGGT-CCATGG	TTGGT-CCATGG	() () () () () () () () () ()
8082	1	G	G	G	GB	GC-AG	GB	G	0	T	ACT	ACT	GC	TC-AC-	TCC-	AA-GC-	AA-GC-	
SEQ ID	271	272	273	274	275	276	83	85	87	277	83	91	93	95	97	66	101	105
Туре	4c	4c	4°	4c	4 e	49	4 7	41	4m	5 a	7a	7c	7d	9a	10a	11a	11a	נן
Isolate	GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	PD19

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8181	CCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTC	ATACTGACTGTAA	TATC-ATCTTGAA	GAT-GAA-AGTAA	AT-GAAGTAA	ATT-GAAGTGAA	CTTAATCAA	TGAA	ATAA	ATG-GATTAGAAGTA-A	-GATATTGAAGTA	GAA-A	GTTG-GATCTAATGCA-T	AATG-GATTATCAATCA	AT-GAGCA-GGCA-T	AGTG-GAATTCATCA-T	.AATCACAGTGCGAAGC	AA-ACTACTA-A-CA-GTGT	CA-AGTGCTGCT
8132	CCCTC		L	B	1 1 1			1 1 1 1	1 1 1 1	A	A-G	A	A	A	L-	A	AA	-AA-A	-AA
	264	265	266	23	22	57	61	63	67	267	268	69	71	73	77	79	569	270	81
	la	1p	1b	1d	1d	1q	1e	1 £	1 9	2a	2 p	2е	2£	2h	2k	21	3a	3b	39
	HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	$_{ m T1}$	T9	PAK64

Isolate Type SEQ ID

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Isolate Type SEQ ID



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Isolate

CAGGACTGCACCATGCTCGTGTGGCGACGACTTAGTCGTTATCTGTGA Type SEQ ID 264 265 265 266 266 61 61 77 77 77 77 77 77 81 HCV-1 HCV-J BE90 BNL1 BNL2 FR1 7 FR2 FR2 FR2 HC-J6 HC-J6 HC-J8 BNL3 FR4 BNL3 FR4 BNL3 FR4 T1

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8182	AGA	AGA	AGAC-GC-ATC-GC-A	AGA	AT	A-A-GT	AGA	A-A	AT		A	A-AAP	A-AAT	ACAT-P	A-AA-TCC	GTACC	D9DD	GTTCCAGTGC
SEQ	271	272	273	274	275	276	83	85	87	277	89	91	93	95	97	66	101	105
Туре	4	4°C	4°C	4°C	4 e	49	4 7	41	4m	5a	7a	7c	7d	9a	10a	11a	11a	11a
Isolate	GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19



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8232	GCGGGGTCCAGGACGCGGCGAGCCTGAGAGC	AACA-	1 1 1 1 1	A	GT-TAACT	GT	GCAAC-GA-CGA	GCAATAA-GA-CGA-AT	rcaa	GTCACTGA-CGA-AT-	GTCAAAC-GT-A-CGAT-	GTCAACTGAGA-AAC-AC-T	GTCAAC-GA-CGA-ATT-	GATCG-TTAGAAGC	TGCCGAGAAGCTC	GTIGC-KCIG-TG-ATAG-GCAGC
SEQ ID	264	266	22.0	57	61 63	67	267	268	69	71	73	77	79	269	270	81
Туре	1a 1b	11p	1q	1d	ıt E	1g	2a	2 p	2e	2£	2h	2k	21	3а	3р	3g
Isolate	HCV-1	BE90 BNI.1	BNL2	FR17	CAMIU/8 FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64

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8271	CG	AAACGAGCCG AAACGAGCCGT-	AAACGAGCCG	TAAGAGCCC	TAACCGAGCCCN	TT-CCAACCCC	CGCCGAGCCCAT	TAAA	A-TAGTGCACT	T-TT-ACGCCA	C-G-G-CL-	TATCT-AC	AA-AGCGC-TT	CA-CG-GAACT-	CA-CGAGAAC	CAACGAGAACNT-
8232	-ATC	GATCAG	GATCTG	GGCCAG	GATCAG	GAAG	GATCGG-C	GCAACGC	GTTTTC	GT-GAATCT	GGAACT	GTTAA-C	GTAAG-T-	AAGG	GAAAG	AAGG
SEQ	271	273	274	276	83	85	87	277	89	91	93	95	97	99	101	105
Туре	7 t	4 4 0 0	4 4 D 0	4	4 K	41	4m	Sa	7a	7c	7d	9a	10a	11a	11a	11a
Isolate	GB48	GB215	GB358 GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19

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7090	VAIKSLTERLYVGGPLTNSRGENCG 2RK-Q	KK	KK-Q	KRIK-Q		LV-HMK-QS	LH	rH	TH	LH	KHIMHI	K-W	IV-HIIK-QS				KSAIMYK-LQ	R
7.645	STVTESDIRTEEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCG	NA-E1 NXSNXE1	NV-SH-EKI	XXVXSA-EKR	RSRA-S-PEE-HJ	RSA-S-PQE1	S-S	RSLA-S-PETH	RXSA-S-PE1	RSLA-S-PE1	A-RSLA-S-PE1	RVSV-LS-S-PEE!	RNS-FLA-S-PEE1				HBB	QVEE-ER
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Type	1a 1b	ק ק דק ק	1d	1£	2 a	5 p	2C	2q	Зe	2£	2h	2k	21	3a	3а	3a	3p	39
Isolate	HCV-1 HCV-J	BNL1 BNL2 BNL2	FR17 CAM1078	FR2 FR16	HC-J6	HC-J8	ARG8	NE92	BNL3	FR4	BNL5	FR13	FR18	BR34	BR36	BR33	T9	PAK64

Fig. 6A NSSB amino acid alignment



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GB48 4c GB116 4c	4 4 0 0	289 290	9KVEVE-EKTAMHK-DL 0KVEVE-ERTAMHDL
GB215	4c	291	KVEVE-EKV-TAMHK-DL
GB358	4°	292	KVEVE-EKTAMHK-DL
GB809	4 e	293	RKVEVE-EKV-AAMHK-DL
CAMG22	4 £	294	RVEVE-ET-KV-SAMHDL
GB549	49	295	R
GB438	4 h	296	RVEE-E-EKV-SAKMYK-DL
CAR4/12	054i	297	PR-X-VEVN-EXDX-KV-NA
CAR1/50	1 4j	298	X-RGEVE-EKV-TAMFK-DL
EG13	4.5	299	VN - E - EKTA MHK - DL
BNL8	4 k	84	KPEVE-EKV-TAMHK-DL
BNL12	41	98	KVEX-EKSAXLMYKL
EG81	4m	88	RVEVE-EKSAMFK-DL
BE95	Sa	300	HMSSQ-EARQCMYK-QO
CHR18	5a	301	HMSSLY-Q-ERQCMYK-00
VN13	7a	90	R-VQHDK-E-ATTDXMXK-QA
VN4	7c	92	RXHDQVKTCXMMQS
VN12	7d	94	-SRHDQVKTCMYQS
FR1	9a	96	GRXDLS-QEK
NE98	10a	86	QV-LS-F-AKDERV-TCMFK-QH
FR14	11a	100	RK-DS-Q-PEEK
FR15	11a	102	RS-XXA-Q-PEEK
FR19	11a	106	R



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Isolate Type SEQ

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	278	279	280	54	26	28	62	64	89	281	282	283	284	70	72	74	78	80	285	286	287	288	82
						1d																	39
	HCV-1	HCV-J	2TY4	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	ARG8	NE92	BNL3	FR4	BNL5	FR13	FR18	BR34	BR36	BR33	T9	PAK64



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2745 2757	SAGVQEDAASLRA		VNB	1	-V-T		-Q-TEERN	-	ŀ	-QEDRN-	-Q-AEERNV	-Q-TEERNV	-Q-TER-ENNP	-Q-TEERNV	1	1	1	-CER-A	-CX-D-EDRAALR
SEQID	278	0 4	56	28	62	68	œ	282	α	70	72	74	78	80	œ	286	α	288	
Type	1a	12.5	1g	1g	- H - H - H	1d	2a	2 p	2d	2 е	2£	2h	2k	21	3a	3а	3a	3b	3g
Isolate	HCV-1	0 -	BNL2	R17	CAM1078	FR16	HC-J6	HC-J8	NE92	BNL3	FR4	BNL5	FR13	FR18	BR34	BR36	BR33	T9	PAK64



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-D-E-KRP-GD-E-KRA-GD-E-KRA-GG-E-KRX-GG-E-KRX-GG-E-KRX-GG-E-KRX-GG-E-KRX-GG-E-KRX-GG-E-KRA-GG-E-KRA-GG-E-KRA-GG-E-R
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